(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
2 September 2004 (02.09.2004)

PCT

(10) International Publication Number
WO 2004/074462 A2

(51) International Patent Classification[7]: C12N

(21) International Application Number:
PCT/US2004/005829

(22) International Filing Date: 20 February 2004 (20.02.2004)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

60/448,632	20 February 2003 (20.02.2003)	US
60/448,633	20 February 2003 (20.02.2003)	US
60/448,797	20 February 2003 (20.02.2003)	US
60/448,806	20 February 2003 (20.02.2003)	US
60/448,810	20 February 2003 (20.02.2003)	US
60/448,812	20 February 2003 (20.02.2003)	US
10/782,141	19 February 2004 (19.02.2004)	US
10/782,096	19 February 2004 (19.02.2004)	US
10/781,979	19 February 2004 (19.02.2004)	US
10/783,417	19 February 2004 (19.02.2004)	US
10/782,020	19 February 2004 (19.02.2004)	US
10/782,570	19 February 2004 (19.02.2004)	US

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(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:
— *without international search report and to be republished upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 2004/074462 A2

(54) Title: DELTA-ENDOTOXIN GENES AND METHODS FOR THEIR USE

(57) Abstract: Compositions and methods for conferring pesticidal activity to bacteria, plants, plant cells, tissues and seeds are provided. Compositions comprising a coding sequence for a delta-endotoxin and delta-endotoxin-associated polypeptides are provided. The coding sequences can be used in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. Compositions also comprise transformed bacteria, plants, plant cells, tissues, and seeds. In particular, isolated delta-endotoxin and delta-endotoxin-associated nucleic acid molecules are provided. Additionally, amino acid sequences corresponding to the polynucleotides are encompassed. In particular, the present invention provides for isolated nucleic acid molecules comprising nucleotide sequences encoding the amino acid sequences shown in in SEQ ID NOS:3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 27, and 29, and the nucleotide sequences set forth in SEQ ID NOS:1, 2, 4, 6, 8, 10, 12, 13, 15, 17, 19, 21, 23, 25, 26, and 28, as well as variants and fragments thereof.

DELTA-ENDOTOXIN GENES AND METHODS FOR THEIR USE

FIELD OF THE INVENTION

This invention relates to the field of molecular biology. Provided are novel genes that encode pesticidal proteins. These proteins and the nucleic acid sequences that encode them are useful in preparing pesticidal formulations and in the production of transgenic pest-resistant plants.

BACKGROUND OF THE INVENTION

Bacillus thuringiensis is a Gram-positive spore forming soil bacterium characterized by its ability to produce crystalline inclusions that are specifically toxic to certain orders and species of insects, but are harmless to plants and other non-targeted organisms. For this reason, compositions including *Bacillus thuringiensis* strains or their insecticidal proteins can be used as environmentally acceptable insecticides to control agricultural insect pests or insect vectors for a variety of human or animal diseases.

Crystal (Cry) proteins (delta-endotoxins) from *Bacillus thuringiensis* have potent insecticidal activity against predominantly Lepidopteran, Dipteran, and Coleopteran larvae. These proteins also have shown activity against Hymenoptera, Homoptera, Phthiraptera, Mallophaga, and Acari pest orders, as well as other invertebrate orders such as Nemathelminthes, Platyhelminthes, and Sarcomastigorphora (Feitelson (1993) The Bacillus Thuringiensis family tree. *In* Advanced Engineered Pesticides. Marcel Dekker, Inc., New York, N.Y.) These proteins were originally classified as CryI to CryV based primarily on their insecticidal activity. The major classes were Lepidoptera-specific (I), Lepidoptera- and Diptera-specific (II), Coleoptera-specific (III), Diptera-specific (IV), and nematode-specific (V) and (VI). The proteins were further classified into subfamilies; more highly related proteins within each family were assigned divisional letters such

as Cry1A, Cry1B, Cry1C, etc. Even more closely related proteins within each division were given names such as Cry1C1, Cry1C2, etc.

A new nomenclature was recently described for the Cry genes based upon amino acid sequence homology rather than insect target specificity (Crickmore *et al.* (1998) *Microbiol. Mol. Biol. Rev.* 62:807-813). In the new classification, each toxin is assigned a unique name incorporating a primary rank (an Arabic number), a secondary rank (an uppercase letter), a tertiary rank (a lowercase letter), and a quaternary rank (another Arabic number). In the new classification, Roman numerals have been exchanged for Arabic numerals in the primary rank. Proteins with less than 45% sequence identity have different primary ranks, and the criteria for secondary and tertiary ranks are 78% and 95%, respectively.

The crystal protein does not exhibit insecticidal activity until it has been ingested and solubilized in the insect midgut. The ingested protoxin is hydrolyzed by proteases in the insect digestive tract to an active toxic molecule. (Höfte and Whiteley (1989) *Microbiol. Rev.* 53:242-255). This toxin binds to apical brush border receptors in the midgut of the target larvae and inserts into the apical membrane creating ion channels or pores, resulting in larval death.

Delta-endotoxins generally have five conserved sequence domains, and three conserved structural domains (see, for example, de Maagd *et al.* (2001) *Trends Genetics* 17:193-199). The first conserved structural domain consists of seven alpha helices and is involved in membrane insertion and pore formation. Domain II consists of three beta-sheets arranged in a Greek key configuration, and domain III consists of two antiparallel beta-sheets in 'jelly-roll' formation (de Maagd *et al.* (2001) supra). Domains II and III are involved in receptor recognition and binding, and are therefore considered determinants of toxin specificity.

Because of the devastation that insects can confer, there is a continual need to discover new forms of *Bacillus thuringiensis* delta-endotoxins.

SUMMARY OF INVENTION

Compositions and methods for conferring pesticide resistance to bacteria, plants, plant cells, tissues, and seeds are provided. Compositions include isolated nucleic acid molecules encoding sequences for delta-endotoxin and delta-endotoxin-associated polypeptides, vectors comprising those nucleic acid molecules, and host

cells comprising the vectors. Compositions also include isolated or recombinant polypeptide sequences of the endotoxin, compositions comprising these polypeptides, and antibodies to those polypeptides. The nucleotide sequences can be used in DNA constructs or expression cassettes for transformation and expression in organisms, including microorganisms and plants. The nucleotide or amino acid sequences may be synthetic sequences that have been designed for optimum expression in an organism, including, but not limited to, a microorganism or a plant. Compositions also comprise transformed bacteria, plants, plant cells, tissues, and seeds.

In particular, the present invention provides for isolated nucleic acid molecules comprising a nucleotide sequence encoding an amino acid sequence shown in SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 27, or 29, or a nucleotide sequence set forth in SEQ ID NO:1, 2, 4, 6, 8, 10, 12, 13, 15, 17, 19, 21, 23, 25, 26, or 28, as well as variants and fragments thereof. Nucleotide sequences that are complementary to a nucleotide sequence of the invention, or that hybridize to a sequence of the invention, are also encompassed.

Methods are provided for producing the polypeptides of the invention, and for using those polypeptides for controlling or killing a lepidopteran or coleopteran pest.

The compositions and methods of the invention are useful for the production of organisms with pesticide resistance, specifically bacteria and plants. These organisms and compositions derived from them are desirable for agricultural purposes. The compositions of the invention are also useful for generating altered or improved delta-endotoxin or delta-endotoxin-associated proteins that have pesticidal activity, or for detecting the presence of delta-endotoxin or delta-endotoxin-associated proteins or nucleic acids in products or organisms.

DESCRIPTION OF FIGURES

Figure 1 shows an alignment of AXMI-004 (SEQ ID NO:3) with cry1Ac (SEQ ID NO:31), cry1Ca (SEQ ID NO:32), cry2Aa (SEQ ID NO:34), cry3Aa1 (SEQ ID NO:35), cry1Ia (SEQ ID NO:33), and cry7Aa (SEQ ID NO:41). Toxins having C-terminal non-toxic domains were artificially truncated as shown. The alignment shows the most highly conserved amino acid residues highlighted in black, and highly conserved amino acid residues highlighted in gray. Conserved group 1 is found from about amino acid residue 174 to about 196 of SEQ ID NO:3. Conserved group 2 is

found from about amino acid residue 250 to about 292 of SEQ ID NO:3. Conserved group 3 is found from about amino acid residue 476 to about 521 of SEQ ID NO:3. Conserved group 4 is found from about amino acid residue 542 to about 552 of SEQ ID NO:3. Conserved group 5 is found from about amino acid residue 618 to about 628 of SEQ ID NO:3

Figures 2A, B, and C show an alignment of AXMI-006 (SEQ ID NO:7) with cry1Aa (SEQ ID NO:30), cry1Ac (SEQ ID NO:31), cry1Ia (SEQ ID NO:33), cry3Aa1 (SEQ ID NO:35), cry3Ba (SEQ ID NO:36), cry 4Aa (SEQ ID NO:38), cry6Aa (SEQ ID NO:40), cry7Aa (SEQ ID NO:41), cry8Aa (SEQ ID NO:42), cry10Aa (SEQ ID NO:43), cry16Aa (SEQ ID NO:44), cry19Ba (SEQ ID NO:45), and cry24Aa (SEQ ID NO:47). Toxins having C-terminal non-toxic domains were artificially truncated as shown. The alignment shows the most highly conserved amino acid residues highlighted in black, and highly conserved amino acid residues highlighted in gray. Conserved group 1 is found from about amino acid residue 218 to about 239 of SEQ ID NO:7. Conserved group 2 is found from about amino acid residue 300 to about 350 of SEQ ID NO:7. Conserved group 3 is found from about amino acid residue 547 to about 592 of SEQ ID NO:7. Conserved group 4 is found from about amino acid residue 611 to about 621 of SEQ ID NO:7. Conserved group 5 is found from about amino acid residue 694 to about 704 of SEQ ID NO:7.

Figures 3A, B, and C show an alignment of AXMI-007 (SEQ ID NO:9) with cry1Aa (SEQ ID NO:30), cry1Ac (SEQ ID NO:31), cry1Ia (SEQ ID NO:33), cry3Aa1 (SEQ ID NO:35), cry3Ba (SEQ ID NO:36), cry 4Aa (SEQ ID NO:38), cry6Aa (SEQ ID NO:40), cry7Aa (SEQ ID NO:41), cry8Aa (SEQ ID NO:42), cry10Aa (SEQ ID NO:43), cry16Aa (SEQ ID NO:44), cry19Ba (SEQ ID NO:45), and cry24Aa (SEQ ID NO:47). Toxins having C-terminal non-toxic domains were artificially truncated as shown. The alignment shows the most highly conserved amino acid residues highlighted in black, and highly conserved amino acid residues highlighted in gray. Conserved group 1 is found from about amino acid residue 217 to about 238 of SEQ ID NO:9. Conserved group 2 is found from about amino acid residue 299 to about 347 of SEQ ID NO:9. Conserved group 3 is found from about amino acid residue 445 to about 590 of SEQ ID NO:9. Conserved group 4 is found from about amino acid

residue 609 to about 619 of SEQ ID NO:9. Conserved group 5 is found from about amino acid residue 692 to about 702 of SEQ ID NO:9.

Figures 4A, B, and C show an alignment of AXMI-008 (SEQ ID NO:14) with cry1Aa (SEQ ID NO:30), cry1Ac (SEQ ID NO:31), cry1Ia (SEQ ID NO:33), cry2Aa (SEQ ID NO:34), cry3Aa1 (SEQ ID NO:35), cry3Bb (SEQ ID NO:37), cry4Aa (SEQ ID NO:38), cry4Ba (SEQ ID NO:39), cry6Aa (SEQ ID NO:40), cry7Aa (SEQ ID NO:41), cry8Aa (SEQ ID NO:42), cry10Aa (SEQ ID NO:43), cry16Aa (SEQ ID NO:44), cry19Ba (SEQ ID NO:45), cry24Aa (SEQ ID NO:47), cry25Aa (SEQ ID NO:48), cry39Aa1 (SEQ ID NO:49), and cry40Aa1 (SEQ ID NO:51). Toxins having C-terminal non-toxic domains were artificially truncated as shown. The alignment shows the most highly conserved amino acid residues highlighted in black, and highly conserved amino acid residues highlighted in gray. Conserved group 1 is found from about amino acid residue 185 to about 206 of SEQ ID NO:14. Conserved group 2 is found from about amino acid residue 276 to about 318 of SEQ ID NO:14. Conserved group 3 is found from about amino acid residue 497 to about 547 of SEQ ID NO:14. Conserved group 4 is found from about amino acid residue 576 to about 586 of SEQ ID NO:14. Conserved group 5 is found from about amino acid residue 657 to about 667 of SEQ ID NO:14.

Figures 5A and B show an alignment of AXMI-008orf2 (SEQ ID NO:18) with cry19Aa-orf2 (SEQ ID NO:46), crybun2-orf2 (SEQ ID NO:50), crybun3-orf2 (SEQ ID NO:52), cry4Aa (SEQ ID NO:38), and cry4Ba (SEQ ID NO:39). The alignment shows the most highly conserved amino acid residues highlighted in black, and highly conserved amino acid residues highlighted in gray.

Figures 6A, B, and C show an alignment of AXMI-009 (SEQ ID NO:20) with cry1Aa (SEQ ID NO:30), cry1Ac (SEQ ID NO:31), cry1Ca (SEQ ID NO:32), cry1Ia (SEQ ID NO:33), cry3Aa1 (SEQ ID NO:35), cry3Ba (SEQ ID NO:36), cry3Bb (SEQ ID NO:37), cry4Aa (SEQ ID NO:38), cry6Aa (SEQ ID NO:40), cry7Aa (SEQ ID NO:41), cry8Aa (SEQ ID NO:42), cry10Aa (SEQ ID NO:43), cry16Aa (SEQ ID NO:44), cry19Ba (SEQ ID NO:45), cry24Aa (SEQ ID NO:47), cry25Aa (SEQ ID NO:48), cry40Aa1 (SEQ ID NO:51). Toxins having C-terminal non-toxic domains

were artificially truncated as shown. The alignment shows the most highly conserved amino acid residues highlighted in black, and highly conserved amino acid residues highlighted in gray. Conserved group 1 is found from about amino acid residue 196 to about 217 of SEQ ID NO:20. Conserved group 2 is found from about amino acid residue 269 to about 311 of SEQ ID NO:20. Conserved group 3 is found from about amino acid residue 514 to about 556 of SEQ ID NO:20. Conserved group 4 is found from about amino acid residue 574 to about 584 of SEQ ID NO:20. Conserved group 5 is found from about amino acid residue 651 to about 661 of SEQ ID NO:20.

Figures 7A, B, and C show an alignment of AXMI-014 (SEQ ID NO:27) with cry1Aa (SEQ ID NO:30), cry1Ac (SEQ ID NO:31), cry1Ia (SEQ ID NO:33), cry2Aa (SEQ ID NO:34), cry3Aa1 (SEQ ID NO:35), cry3Bb (SEQ ID NO:37), cry4Aa (SEQ ID NO:38), cry4Ba (SEQ ID NO:39), cry6Aa (SEQ ID NO:40), cry7Aa (SEQ ID NO:41), cry8Aa (SEQ ID NO:42), cry10Aa (SEQ ID NO:43), cry16Aa (SEQ ID NO:44), cry19Ba (SEQ ID NO:45), cry24Aa (SEQ ID NO:47), cry25Aa (SEQ ID NO:48), cry39Aa1 (SEQ ID NO:49), and cry40Aa1 (SEQ ID NO:51). Toxins having C-terminal non-toxic domains were artificially truncated as shown. The alignment shows the most highly conserved amino acid residues highlighted in black, and highly conserved amino acid residues highlighted in gray. Conserved group 1 is found from about amino acid residue 177 to about 188 of SEQ ID NO:27. Conserved group 2 is found from about amino acid residue 251 to about 293 of SEQ ID NO:27. Conserved group 3 is found from about amino acid residue 483 to about 533 of SEQ ID NO:27. Conserved group 4 is found from about amino acid residue 552 to about 562 of SEQ ID NO:27.

Figure 8 shows a photograph of a 4-20% gradient SDS acrylamide gel. Lanes 1-4 contain various concentrations of sporulated *Bacillus* cell culture expressing 69 kD AXMI-004 protein. Lanes 5-8 contain various concentrations of BSA. Lane 9 contains a size marker. An arrow indicates the 69 kD band.

DETAILED DESCRIPTION

The present invention is drawn to compositions and methods for regulating pest resistance in organisms, particularly plants or plant cells. The methods involve

transforming organisms with a nucleotide sequence encoding a delta-endotoxin or delta-endotoxin-associated protein of the invention. In particular, the nucleotide sequences of the invention are useful for preparing plants and microorganisms that possess pesticidal activity. Thus, transformed bacteria, plants, plant cells, plant tissues and seeds are provided. Compositions are delta-endotoxin or delta-endotoxin-associated nucleic acids and proteins of *Bacillus thuringiensis*. The sequences find use in the construction of expression vectors for subsequent transformation into organisms of interest, as probes for the isolation of other delta-endotoxin or delta-endotoxin-associated genes, and for the generation of altered pesticidal proteins by methods known in the art, such as domain swapping or DNA shuffling. The proteins find use in controlling or killing lepidopteran or coleopteran pest populations and for producing compositions with pesticidal activity.

Definitions

By "delta-endotoxin" is intended a toxin from *Bacillus thuringiensis* that has toxic activity against one or more pests, including, but not limited to, members of the Lepidoptera, Diptera, and Coleoptera orders. In some cases, delta-endotoxin proteins have been isolated from other organisms, including *Clostridium bifermentans* and *Paenibacillus popilliae*. Delta-endotoxin proteins include amino acid sequences deduced from the full-length nucleotide sequences disclosed herein, and amino acid sequences that are shorter than the full-length sequences, either due to the use of an alternate downstream start site, or due to processing that produces a shorter protein having pesticidal activity. Processing may occur in the organism the protein is expressed in, or in the pest after ingestion of the protein. Delta-endotoxins include proteins identified as cry1 through cry43, cyt1 and cyt2, and Cyt-like toxin. There are currently over 250 known species of delta-endotoxins with a wide range of specificities and toxicities. For an expansive list see Crickmore *et al.* (1998), *Microbiol. Mol. Biol. Rev.* 62:807-813, and for regular updates see Crickmore *et al.* (2003) "*Bacillus thuringiensis* toxin nomenclature," at www.biols.susx.ac.uk/Home/Neil_Crickmore/Bt/index.

Bacterial genes, such as the AXMI genes of this invention, quite often possess multiple methionine initiation codons in proximity to the start of the open reading frame. Often, translation initiation at one or more of these start codons will lead to

generation of a functional protein. These start codons can include ATG codons. However, bacteria such as *Bacillus sp.* also recognize the codon GTG as a start codon, and proteins that initiate translation at GTG codons contain a methionine at the first amino acid. Furthermore, it is not often determined *a priori* which of these codons are used naturally in the bacterium. Thus, it is understood that use of one of the alternate methionine codons may also lead to generation of delta-endotoxin proteins that encode pesticidal activity. For example, an alternate start site for an AXMI-004 delta-endotoxin protein of the invention is at base pair 385 of SEQ ID NO:1. Translation from this alternate start site results in the amino acid sequence found in SEQ ID NO:5. An alternate start site for an AXMI-007 delta-endotoxin protein of the invention may be at base pair 151 of SEQ ID NO:8. Translation from this alternate start site results in the amino acid sequence found in SEQ ID NO:11. An alternate start site for an AXMI-008 delta-endotoxin protein of the invention may be at nucleotide 177 of SEQ ID NO:12. Translation from this alternate start site results in the amino acid sequence found in SEQ ID NO:16. An alternate start site for an AXMI-009 delta-endotoxin protein of the invention may be at nucleotide 34 of SEQ ID NO:19. Translation from this alternate start site results in the amino acid sequence found in SEQ ID NO:22. An additional alternate start site for an AXMI-009 delta-endotoxin protein of the invention may be at nucleotide 64 of SEQ ID NO:1. Translation from this alternate start site results in the amino acid sequence found in SEQ ID NO:24. An alternate start site for an AXMI-014 delta-endotoxin protein of the invention may be at base pair 136 of SEQ ID NO:25. Translation from this alternate start site results in the amino acid sequence found in SEQ ID NO:29. These delta-endotoxin proteins are encompassed in the present invention and may be used in the methods of the present invention.

In addition, there may be one or more additional open reading frames in the disclosed nucleotide sequences that encode one or more delta-endotoxin-associated proteins. By "delta-endotoxin-associated protein" is intended a protein encoded by a nucleotide sequence disclosed herein using an alternate open reading frame than that used by the delta-endotoxins of the present invention. Proteins such as these are known in the art as helper proteins, stabilizing sequences, or delta-endotoxin-associated proteins. These delta-endotoxin-associated proteins may have pesticidal activity, or may be important in facilitating expression of delta-endotoxin proteins.

Methods are known in the art for measuring pesticidal activity and for determining the effects of delta-endotoxin-associated proteins on delta-endotoxin protein expression and crystal formation (see, for example, Park *et al.* (1999) *FEMS Microbiol. Lett.* 181:319-327; Ge *et al.* (1998) *FEMS Microbiol. Lett.* 165:35-41; Rosso and Delecluse (1997) *Appl. Environ. Microbiol.* 63:4449-4455). These delta-endotoxin-associated proteins are encompassed by the present invention, and may be used in the methods disclosed herein, either alone or in combination with known delta-endotoxin proteins. In one embodiment, the delta-endotoxin-associated protein has the amino acid sequence found in SEQ ID NO:18 and is encoded by the nucleotide sequence of SEQ ID NO:17.

By "plant cell" is intended all known forms of plant, including undifferentiated tissue (e.g. callus), suspension culture cells, protoplasts, leaf cells, root cells, phloem cells, plant seeds, pollen, propagules, embryos and the like. By "plant expression cassette" is intended a DNA construct that is capable of resulting in the expression of a protein from an open reading frame in a plant cell. Typically these contain a promoter and a coding sequence. Often, such constructs will also contain a 3' untranslated region. Such constructs may contain a 'signal sequence' or 'leader sequence' to facilitate co-translational or post-translational transport of the peptide to certain intracellular structures such as the chloroplast (or other plastid), endoplasmic reticulum, or Golgi apparatus.

By "signal sequence" is intended a sequence that is known or suspected to result in cotranslational or post-translational peptide transport across the cell membrane. In eukaryotes, this typically involves secretion into the Golgi apparatus, with some resulting glycosylation. By "leader sequence" is intended any sequence that when translated, results in an amino acid sequence sufficient to trigger co-translational transport of the peptide chain to a sub-cellular organelle. Thus, this includes leader sequences targeting transport and/or glycosylation by passage into the endoplasmic reticulum, passage to vacuoles, plastids including chloroplasts, mitochondria, and the like.

By "plant transformation vector" is intended a DNA molecule that is necessary for efficient transformation of a plant cell. Such a molecule may consist of one or more plant expression cassettes, and may be organized into more than one 'vector' DNA molecule. For example, binary vectors are plant transformation vectors

that utilize two non-contiguous DNA vectors to encode all requisite cis- and trans-acting functions for transformation of plant cells (Hellens and Mullineaux (2000) *Trends in Plant Science* 5:446-451). "Vector" refers to a nucleic acid construct designed for transfer between different host cells. "Expression vector" refers to a vector that has ability to incorporate, integrate and express heterologous DNA sequences or fragments in a foreign cell.

"Transgenic plants" or "transformed plants" or "stably transformed plants or cells or tissues" refers to plants that have incorporated or integrated exogenous nucleic acid sequences or DNA fragments into the plant cell. These nucleic acid sequences include those that are exogenous, or not present in the untransformed plant cell, as well as those that may be endogenous, or present in the untransformed plant cell. "Heterologous" generally refers to the nucleic acid sequences that are not endogenous to the cell or part of the native genome in which they are present, and have been added to the cell by infection, transfection, microinjection, electroporation, microprojection, or the like.

"Promoter" refers to a nucleic acid sequence that functions to direct transcription of a downstream coding sequence. The promoter together with other transcriptional and translational regulatory nucleic acid sequences (also termed "control sequences") are necessary for the expression of a DNA sequence of interest.

Provided herein are novel isolated nucleotide sequences that confer pesticidal activity. Also provided are the amino acid sequences for the delta-endotoxin and delta-endotoxin-associated proteins. The protein resulting from translation of this gene allows cells to control or kill pests that ingest it.

An "isolated" or "purified" nucleic acid molecule or protein, or biologically active portion thereof, is substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized. Preferably, an "isolated" nucleic acid is free of sequences (preferably protein encoding sequences) that naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For purposes of the invention, "isolated" when used to refer to nucleic acid molecules excludes isolated chromosomes. For example, in various embodiments, the isolated delta-endotoxin or delta-endotoxin-associated-encoding nucleic acid

molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb, or 0.1 kb of nucleotide sequence that naturally flanks the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. A delta-endotoxin or delta-endotoxin-associated protein that is substantially free of cellular material includes preparations of protein having less than about 30%, 20%, 10%, or 5% (by dry weight) of non-delta-endotoxin or non-delta-endotoxin-associated protein (also referred to herein as a "contaminating protein"). Various aspects of the invention are described in further detail in the following subsections.

Isolated Nucleic Acid Molecules, and Variants and Fragments Thereof

One aspect of the invention pertains to isolated nucleic acid molecules comprising nucleotide sequences encoding delta-endotoxin or delta-endotoxin-associated proteins and polypeptides or biologically active portions thereof, as well as nucleic acid molecules sufficient for use as hybridization probes to identify delta-endotoxin or delta-endotoxin-associated-encoding nucleic acids. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (e.g., cDNA or genomic DNA) and RNA molecules (e.g., mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA.

Nucleotide sequences encoding the proteins of the present invention include the sequences set forth in SEQ ID NOS:1, 2, 4, 6, 8, 10, 12, 13, 15, 17, 19, 21, 23, 25, 26, and 28, and complements thereof. By "complement" is intended a nucleotide sequence that is sufficiently complementary to a given nucleotide sequence such that it can hybridize to the given nucleotide sequence to thereby form a stable duplex. The corresponding amino acid sequences for the delta-endotoxin or delta-endotoxin-associated proteins encoded by these nucleotide sequences are set forth in SEQ ID NOS:3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 27, and 29.

Nucleic acid molecules that are fragments of these delta-endotoxin or delta-endotoxin-associated protein-encoding nucleotide sequences are also encompassed by the present invention. By "fragment" is intended a portion of the nucleotide sequence encoding a delta-endotoxin protein or delta-endotoxin-associated protein. A fragment of a nucleotide sequence may encode a biologically active portion of a delta-endotoxin or delta-endotoxin-associated protein, or it may be a fragment that can be

used as a hybridization probe or PCR primer using methods disclosed below. Nucleic acid molecules that are fragments of a delta-endotoxin or a delta-endotoxin-associated nucleotide sequence comprise at least about 15, 20, 50, 75, 100, 200, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, 2100, 2200, 2300, 2400, 2500, 3000, 3500, 4000, 4500, 5000, 5500 nucleotides, or up to the number of nucleotides present in a full-length delta-endotoxin or delta-endotoxin-associated protein-encoding nucleotide sequence disclosed herein (for example, 2190 nucleotides for SEQ ID NO:1, 1890 for SEQ ID NO:2, etc.), depending upon the intended use.

Fragments of the nucleotide sequences of the present invention will encode protein fragments that retain the biological activity of the delta endotoxin or delta-endotoxin-associated protein and, hence, retain pesticidal activity or delta-endotoxin-associated protein activity, respectively. By "delta-endotoxin activity" is intended pesticidal activity. By "delta-endotoxin-associated protein activity" is intended that the protein have pesticidal activity, or that the protein improves expression of a delta-endotoxin protein. This improvement in protein expression can happen by any mechanism. By "retains activity" is intended that the fragment will have at least about 30%, preferably at least about 50%, more preferably at least about 70%, even more preferably at least about 80% of the activity of the delta-endotoxin or delta-endotoxin-associated protein. Methods are known in the art for determining the effects of delta-endotoxin-associated proteins on delta-endotoxin protein expression and crystal formation (see, for example, Park *et al.* (1999) *FEMS Microbiol. Lett.* 181:319-327; Ge *et al.* (1998) *FEMS Microbiol. Lett.* 165:35-41; Rosso and Delecluse (1997) *Appl. Environ. Microbiol.* 63:4449-4455). Methods for measuring pesticidal activity are well known in the art. See, for example, Czapla and Lang (1990) *J. Econ. Entomol.* 83(6): 2480-2485; Andrews *et al.* (1988) *Biochem. J.* 252:199-206; Marrone *et al.* (1985) *J. of Economic Entomology* 78:290-293; and U.S. Patent No. 5,743,477, all of which are herein incorporated by reference in their entirety.

A fragment of a delta-endotoxin or delta-endotoxin-associated protein-encoding nucleotide sequence that encodes a biologically active portion of a protein of the invention will encode at least about 15, 25, 30, 50, 75, 100, 125, 150, 175, 200, 250, 300, 350, 400, 450, 500, 550, 600, or 650 contiguous amino acids, or up to the total number of amino acids present in a full-length delta-endotoxin or delta-

endotoxin-associated protein of the invention (for example, 629 amino acids for SEQ ID NO:3, 601 amino acids for SEQ ID NO:5, etc.).

Preferred delta-endotoxin or delta-endotoxin-associated proteins of the present invention are encoded by a nucleotide sequences sufficiently identical to the nucleotide sequences of in SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 27, or 29. By "sufficiently identical" is intended an amino acid or nucleotide sequence that has at least about 60% or 65% sequence identity, preferably about 70% or 75% sequence identity, more preferably about 80% or 85% sequence identity, most preferably about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity compared to a reference sequence using one of the alignment programs described herein using standard parameters. One of skill in the art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning, and the like.

To determine the percent identity of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences (i.e., percent identity = number of identical positions/total number of positions (e.g., overlapping positions) x 100). In one embodiment, the two sequences are the same length. The percent identity between two sequences can be determined using techniques similar to those described below, with or without allowing gaps. In calculating percent identity, typically exact matches are counted.

The determination of percent identity between two sequences can be accomplished using a mathematical algorithm. A nonlimiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-5877. Such an algorithm is incorporated into the BLASTN and BLASTX programs of Altschul *et al.* (1990) *J. Mol. Biol.* 215:403. BLAST nucleotide searches can be performed with the BLASTN program, score = 100, wordlength = 12, to obtain nucleotide sequences homologous to delta-endotoxin or delta-endotoxin-associated nucleic acid molecules of the invention. BLAST protein searches can be performed with the BLASTX

program, score = 50, wordlength = 3, to obtain amino acid sequences homologous to delta-endotoxin or delta-endotoxin-associated protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.* (1997) *Nucleic Acids Res.* 25:3389. Alternatively, PSI-Blast can be used to perform an iterated search that detects distant relationships between molecules. See, Altschul *et al.* (1997) *supra*. When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (e.g., BLASTX and BLASTN) can be used. See, www.ncbi.nlm.nih.gov. Another non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the ClustalW algorithm (Higgins *et al.* (1994) *Nucleic Acids Res.* 22:4673-4680). ClustalW compares sequences and aligns the entirety of the amino acid or DNA sequence, and thus can provide data about the sequence conservation of the entire amino acid sequence. The ClustalW algorithm is used in several commercially available DNA/amino acid analysis software packages, such as the ALIGNX module of the vector NTi Program Suite (Informax, Inc). After alignment of amino acid sequences with ClustalW, the percent amino acid identity can be assessed. A non-limiting example of a software program useful for analysis of ClustalW alignments is GeneDoc™. Genedoc™ (Karl Nicholas) allows assessment of amino acid (or DNA) similarity and identity between multiple proteins. Another non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller (1988) *CABIOS* 4:11-17. Such an algorithm is incorporated into the ALIGN program (version 2.0), which is part of the GCG sequence alignment software package (available from Accelrys, Inc., 9865 Scranton Rd., San Diego, California, USA). When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used.

The invention also encompasses variant nucleic acid molecules. "Variants" of the delta-endotoxin or delta-endotoxin-associated protein-encoding nucleotide sequences include those sequences that encode the delta-endotoxin or delta-endotoxin-associated proteins disclosed herein but that differ conservatively because of the degeneracy of the genetic code as well as those that are sufficiently identical as discussed above. Naturally occurring allelic variants can be identified with the use of well-known molecular biology techniques, such as polymerase chain reaction (PCR)

and hybridization techniques as outlined below. Variant nucleotide sequences also include synthetically derived nucleotide sequences that have been generated, for example, by using site-directed mutagenesis but which still encode the delta-endotoxin or delta-endotoxin-associated proteins disclosed in the present invention as discussed below. Variant proteins encompassed by the present invention are biologically active, that is they continue to possess the desired biological activity of the native protein, that is, retaining pesticidal activity. By "retains activity" is intended that the variant will have at least about 30%, preferably at least about 50%, more preferably at least about 70%, even more preferably at least about 80% of the activity of the delta-endotoxin or delta-endotoxin-associated protein. Methods for measuring pesticidal activity are well known in the art. See, for example, Czapla and Lang (1990) *J. Econ. Entomol.* 83(6): 2480-2485; Andrews *et al.* (1988) *Biochem. J.* 252:199-206; Marrone *et al.* (1985) *J. of Economic Entomology* 78:290-293; and U.S. Patent No. 5,743,477, all of which are herein incorporated by reference in their entirety.

The invention also encompasses variant nucleic acid molecules. "Variants" of the delta-endotoxin or delta-endotoxin-associated-encoding nucleotide sequences include those sequences that encode the delta-endotoxin or delta-endotoxin-associated proteins disclosed herein but that differ conservatively because of the degeneracy of the genetic code as well as those that are sufficiently identical as discussed above. Naturally occurring allelic variants can be identified with the use of well-known molecular biology techniques, such as polymerase chain reaction (PCR) and hybridization techniques as outlined below. Variant nucleotide sequences also include synthetically derived nucleotide sequences that have been generated, for example, by using site-directed mutagenesis but which still encode the delta-endotoxin or delta-endotoxin-associated proteins disclosed in the present invention as discussed below.

The skilled artisan will further appreciate that changes can be introduced by mutation into the nucleotide sequences of the invention thereby leading to changes in the amino acid sequence of the encoded delta-endotoxin or delta-endotoxin-associated proteins, without altering the biological activity of the proteins. Thus, variant isolated nucleic acid molecules can be created by introducing one or more nucleotide substitutions, additions, or deletions into the corresponding nucleotide sequence

disclosed herein, such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Such variant nucleotide sequences are also encompassed by the present invention.

For example, preferably, conservative amino acid substitutions may be made at one or more predicted, preferably nonessential amino acid residues. A "nonessential" amino acid residue is a residue that can be altered from the wild-type sequence of a delta-endotoxin or delta-endotoxin-associated protein without altering the biological activity, whereas an "essential" amino acid residue is required for biological activity. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine).

There are generally five highly conserved regions among the delta-endotoxin proteins, concentrated largely in the center of the domain or at the junction between domains (Rajamohan *et al.* (1998) *Prog. Nucleic Acid Res. Mol. Biol.* 60:1 –23). The blocks of conserved amino acids for various delta-endotoxins as well as consensus sequences may be found in Schnepf *et al.* (1998) *Microbio. Mol. Biol. Rev.* 62:775-806 and Lereclus *et al.* (1989) Role, Structure, and Molecular Organization of the Genes Coding for the Parasporal d-endotoxins of *Bacillus thuringiensis. In* Regulation of Procaryotic Development. Issar Smit, Slepecky, R.A., Setlow, P. American Society for Microbiology, Washington, D.C. 20006. It has been proposed that delta-endotoxins having these conserved regions may share a similar structure, consisting of three domains (Li *et al.* (1991) *Nature* 353: 815-821). Domain I has the highest similarity between delta-endotoxins (Bravo (1997) *J. Bacteriol.* 179:2793-2801).

Amino acid substitutions may be made in nonconserved regions that retain function. In general, such substitutions would not be made for conserved amino acid residues, or for amino acid residues residing within a conserved motif, where such residues are essential for protein activity. Examples of residues that are conserved and that may be essential for protein activity include, for example, residues that are identical between all proteins contained in the alignments provided. Examples of residues that are conserved but that may allow conservative amino acid substitutions and still retain activity include, for example, residues that have only conservative substitutions between all proteins contained in the alignments provided. However, one of skill in the art would understand that functional variants may have minor conserved or nonconserved alterations in the conserved residues.

Alternatively, variant nucleotide sequences can be made by introducing mutations randomly along all or part of the coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for ability to confer delta-endotoxin or delta-endotoxin-associated activity to identify mutants that retain activity. Following mutagenesis, the encoded protein can be expressed recombinantly, and the activity of the protein can be determined using standard assay techniques.

Using methods such as PCR, hybridization, and the like corresponding delta-endotoxin or delta-endotoxin-associated sequences can be identified, such sequences having substantial identity to the sequences of the invention. *See*, for example, Sambrook J., and Russell, D.W. (2001) *Molecular Cloning: A Laboratory Manual.* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY) and Innis, *et al.* (1990) *PCR Protocols: A Guide to Methods and Applications* (Academic Press, NY).

In a hybridization method, all or part of the delta-endotoxin or delta-endotoxin-associated nucleotide sequence can be used to screen cDNA or genomic libraries. Methods for construction of such cDNA and genomic libraries are generally known in the art and are disclosed in Sambrook and Russell, 2001. The so-called hybridization probes may be genomic DNA fragments, cDNA fragments, RNA fragments, or other oligonucleotides, and may be labeled with a detectable group such as ^{32}P, or any other detectable marker, such as other radioisotopes, a fluorescent compound, an enzyme, or an enzyme co-factor. Probes for hybridization can be made by labeling synthetic oligonucleotides based on the known delta-endotoxin or delta-

endotoxin-associated-encoding nucleotide sequence disclosed herein. Degenerate primers designed on the basis of conserved nucleotides or amino acid residues in the nucleotide sequence or encoded amino acid sequence can additionally be used. The probe typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably at least about 50, 75, 100, 125, 150, 175, 200, 250, 300, 350, or 400 consecutive nucleotides of delta-endotoxin or delta-endotoxin-associated-encoding nucleotide sequence of the invention or a fragment or variant thereof. Preparation of probes for hybridization is generally known in the art and is disclosed in Sambrook and Russell, 2001, herein incorporated by reference.

In hybridization techniques, all or part of a known nucleotide sequence is used as a probe that selectively hybridizes to other corresponding nucleotide sequences present in a population of cloned genomic DNA fragments or cDNA fragments (i.e., genomic or cDNA libraries) from a chosen organism. The hybridization probes may be genomic DNA fragments, cDNA fragments, RNA fragments, or other oligonucleotides, and may be labeled with a detectable group such as ^{32}P, or any other detectable marker. Thus, for example, probes for hybridization can be made by labeling synthetic oligonucleotides based on the delta-endotoxin or delta-endotoxin-associated sequence of the invention. Methods for preparation of probes for hybridization and for construction of cDNA and genomic libraries are generally known in the art and are disclosed in Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, New York).

For example, the entire delta-endotoxin or delta-endotoxin-associated sequence disclosed herein, or one or more portions thereof, may be used as a probe capable of specifically hybridizing to corresponding delta-endotoxin or delta-endotoxin-associated-like sequences and messenger RNAs. To achieve specific hybridization under a variety of conditions, such probes include sequences that are unique and are preferably at least about 10 nucleotides in length, and most preferably at least about 20 nucleotides in length. Such probes may be used to amplify corresponding delta-endotoxin or delta-endotoxin-associated sequences from a chosen organism by PCR. This technique may be used to isolate additional coding sequences from a desired organism or as a diagnostic assay to determine the presence of coding

sequences in an organism. Hybridization techniques include hybridization screening of plated DNA libraries (either plaques or colonies; see, for example, Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, New York).

Hybridization of such sequences may be carried out under stringent conditions. By "stringent conditions" or "stringent hybridization conditions" is intended conditions under which a probe will hybridize to its target sequence to a detectably greater degree than to other sequences (e.g., at least 2-fold over background). Stringent conditions are sequence-dependent and will be different in different circumstances. By controlling the stringency of the hybridization and/or washing conditions, target sequences that are 100% complementary to the probe can be identified (homologous probing). Alternatively, stringency conditions can be adjusted to allow some mismatching in sequences so that lower degrees of similarity are detected (heterologous probing). Generally, a probe is less than about 1000 nucleotides in length, preferably less than 500 nucleotides in length.

Typically, stringent conditions will be those in which the salt concentration is less than about 1.5 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides) and at least about 60°C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. Exemplary low stringency conditions include hybridization with a buffer solution of 30 to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulphate) at 37°C, and a wash in 1X to 2X SSC (20X SSC = 3.0 M NaCl/0.3 M trisodium citrate) at 50 to 55°C. Exemplary moderate stringency conditions include hybridization in 40 to 45% formamide, 1.0 M NaCl, 1% SDS at 37°C, and a wash in 0.5X to 1X SSC at 55 to 60°C. Exemplary high stringency conditions include hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 0.1X SSC at 60 to 65°C. Optionally, wash buffers may comprise about 0.1% to about 1% SDS. Duration of hybridization is generally less than about 24 hours, usually about 4 to about 12 hours.

Specificity is typically the function of post-hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. For DNA-DNA hybrids, the T_m can be approximated from the equation of Meinkoth and Wahl

(1984) *Anal. Biochem.* 138:267-284: $T_m = 81.5°C + 16.6 (\log M) + 0.41 (\%GC) - 0.61 (\%$ form) - 500/L; where M is the molarity of monovalent cations, %GC is the percentage of guanosine and cytosine nucleotides in the DNA, % form is the percentage of formamide in the hybridization solution, and L is the length of the hybrid in base pairs. The T_m is the temperature (under defined ionic strength and pH) at which 50% of a complementary target sequence hybridizes to a perfectly matched probe. T_m is reduced by about 1°C for each 1% of mismatching; thus, T_m, hybridization, and/or wash conditions can be adjusted to hybridize to sequences of the desired identity. For example, if sequences with $\geq$90% identity are sought, the T_m can be decreased 10°C. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence and its complement at a defined ionic strength and pH. However, severely stringent conditions can utilize a hybridization and/or wash at 1, 2, 3, or 4°C lower than the thermal melting point (T_m); moderately stringent conditions can utilize a hybridization and/or wash at 6, 7, 8, 9, or 10°C lower than the thermal melting point (T_m); low stringency conditions can utilize a hybridization and/or wash at 11, 12, 13, 14, 15, or 20°C lower than the thermal melting point (T_m). Using the equation, hybridization and wash compositions, and desired T_m, those of ordinary skill will understand that variations in the stringency of hybridization and/or wash solutions are inherently described. If the desired degree of mismatching results in a T_m of less than 45°C (aqueous solution) or 32°C (formamide solution), it is preferred to increase the SSC concentration so that a higher temperature can be used. An extensive guide to the hybridization of nucleic acids is found in Tijssen (1993) *Laboratory Techniques in Biochemistry and Molecular Biology—Hybridization with Nucleic Acid Probes,* Part I, Chapter 2 (Elsevier, New York); and Ausubel *et al.*, eds. (1995) *Current Protocols in Molecular Biology*, Chapter 2 (Greene Publishing and Wiley-Interscience, New York). See Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, New York).

Isolated Proteins and Variants and Fragments Thereof

Delta-endotoxin and delta-endotoxin-associated proteins are also encompassed within the present invention. By "delta-endotoxin protein" is intended a protein having the amino acid sequence set forth in SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 20, 22,

24, 27, or 29. By "delta-endotoxin-associated protein" is intended a protein having the amino acid sequence set forth in SEQ ID NO:18. Fragments, biologically active portions, and variants thereof are also provided, and may be used to practice the methods of the present invention.

"Fragments" or "biologically active portions" include polypeptide fragments comprising a portion of an amino acid sequence encoding a delta-endotoxin or delta-endotoxin-associated protein as set forth in SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 27, or 29, and that retain delta-endotoxin activity or delta-endotoxin-associated activity. A biologically active portion of a delta-endotoxin or delta-endotoxin-associated protein can be a polypeptide that is, for example, 10, 25, 50, 100 or more amino acids in length. Such biologically active portions can be prepared by recombinant techniques and evaluated for delta-endotoxin or delta-endotoxin-associated activity. Methods for measuring pesticidal activity are well known in the art. See, for example, Czapla and Lang (1990) *J. Econ. Entomol.* 83(6): 2480-2485; Andrews *et al.* (1988) *Biochem. J.* 252:199-206; Marrone *et al.* (1985) *J. of Economic Entomology* 78:290-293; and U.S. Patent No. 5,743,477, all of which are herein incorporated by reference in their entirety. As used here, a fragment comprises at least 8 contiguous amino acids SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 27, or 29. The invention encompasses other fragments, however, such as any fragment in the protein greater than about 10, 20, 30, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, and 650 amino acids.

By "variants" is intended proteins or polypeptides having an amino acid sequence that is at least about 60%, 65%, preferably about 70%, 75%, more preferably about 80%, 85%, most preferably about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to the amino acid sequence of SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 27, or 29. Variants also include polypeptides encoded by a nucleic acid molecule that hybridizes to the nucleic acid molecule of SEQ ID NO:1, 2, 4, 6, 8, 10, 12, 13, 15, 17, 19, 21, 23, 25, 26, or 28, or a complement thereof, under stringent conditions. Such variants generally retain delta-endotoxin or delta-endotoxin-associated activity. Variants include polypeptides that differ in amino acid sequence due to mutagenesis. Variant proteins encompassed by the present invention are biologically active, that is they continue to possess the desired biological activity of the native protein, that is, retaining pesticidal activity. Methods for measuring

pesticidal activity are well known in the art. See, for example, Czapla and Lang (1990) *J. Econ. Entomol.* 83(6): 2480-2485; Andrews *et al.* (1988) *Biochem. J.* 252:199-206; Marrone *et al.* (1985) *J. of Economic Entomology* 78:290-293; and U.S. Patent No. 5,743,477, all of which are herein incorporated by reference in their entirety.

Altered or Improved Variants

It is recognized that DNA sequences of a delta-endotoxin or delta-endotoxin-associated protein may be altered by various methods, and that these alterations may result in DNA sequences encoding proteins with amino acid sequences different than that encoded by the delta-endotoxin or delta-endotoxin-associated protein of the present invention. This protein may be altered in various ways including amino acid substitutions, deletions, truncations, and insertions. Methods for such manipulations are generally known in the art. For example, amino acid sequence variants of the delta-endotoxin or delta-endotoxin-associated protein can be prepared by mutations in the DNA. This may also be accomplished by one of several forms of mutagenesis and/or in directed evolution. In some aspects, the changes encoded in the amino acid sequence will not substantially affect the function of the protein. Such variants will possess the desired pesticidal activity. However, it is understood that the ability of a delta-endotoxin or delta-endotoxin-associated protein to confer pesticidal activity may be improved by the use of such techniques upon the compositions of this invention. For example, one may express the delta-endotoxin or delta-endotoxin-associated protein in host cells that exhibit high rates of base misincorporation during DNA replication, such as XL-1 Red (Stratagene). After propagation in such strains, one can isolate the delta-endotoxin or delta-endotoxin-associated DNA (for example by preparing plasmid DNA, or by amplifying by PCR and cloning the resulting PCR fragment into a vector), culture the delta-endotoxin or delta-endotoxin-associated mutations in a non-mutagenic strain, and identify mutated delta-endotoxin or delta-endotoxin-associated genes with pesticidal activity, for example by performing an assay to test for pesticidal activity. Generally, the protein is mixed and used in feeding assays. See, for example Marrone *et al.* (1985) *J. of Economic Entomology* 78:290-293. Such assays can include contacting plants with one or more pests and determining the plant's ability to survive and/or cause the death of the pests.

Examples of mutations that result in increased toxicity are found in Schnepf *et al.* (1998) *Microbiol. Mol. Biol. Rev.* 62:775-806.

Alternatively, alterations may be made to the protein sequence of many proteins at the amino or carboxy terminus without substantially affecting activity. This can include insertions, deletions, or alterations introduced by modern molecular methods, such as PCR, including PCR amplifications that alter or extend the protein coding sequence by virtue of inclusion of amino acid encoding sequences in the oligonucleotides utilized in the PCR amplification. Alternatively, the protein sequences added can include entire protein-coding sequences, such as those used commonly in the art to generate protein fusions. Such fusion proteins are often used to (1) increase expression of a protein of interest (2) introduce a binding domain, enzymatic activity, or epitope to facilitate either protein purification, protein detection, or other experimental uses known in the art (3) target secretion or translation of a protein to a subcellular organelle, such as the periplasmic space of Gram-negative bacteria, or the endoplasmic reticulum of eukaryotic cells, the latter of which often results in glycosylation of the protein.

Variant nucleotide and amino acid sequences of the present invention also encompass sequences derived from mutagenic and recombinogenic procedures such as DNA shuffling. With such a procedure, one or more different delta-endotoxin or delta-endotoxin-associated protein coding regions can be used to create a new delta-endotoxin or delta-endotoxin-associated protein possessing the desired properties. In this manner, libraries of recombinant polynucleotides are generated from a population of related sequence polynucleotides comprising sequence regions that have substantial sequence identity and can be homologously recombined *in vitro* or *in vivo*. For example, using this approach, sequence motifs encoding a domain of interest may be shuffled between the delta-endotoxin or delta-endotoxin-associated gene of the invention and other known delta-endotoxin or delta-endotoxin-associated genes to obtain a new gene coding for a protein with an improved property of interest, such as an increased insecticidal activity. Strategies for such DNA shuffling are known in the art. See, for example, Stemmer (1994) *Proc. Natl. Acad. Sci. USA* 91:10747-10751; Stemmer (1994) *Nature* 370:389-391; Crameri *et al.* (1997) *Nature Biotech.* 15:436-438; Moore *et al.* (1997) *J. Mol. Biol.* 272:336-347; Zhang *et al. (1997) Proc. Natl.*

Acad. Sci. USA 94:4504-4509; Crameri *et al.* (1998) *Nature* 391:288-291; and U.S. Patent Nos. 5,605,793 and 5,837,458.

Domain swapping or shuffling is another mechanism for generating altered delta-endotoxin or delta-endotoxin-associated proteins. Domains II and III may be swapped between delta-endotoxin proteins, resulting in hybrid or chimeric toxins with improved pesticidal activity or target spectrum. Methods for generating recombinant proteins and testing them for pesticidal activity are well known in the art (see, for example, Naimov *et al.* (2001) *Appl. Environ. Microbiol.* 67:5328-5330; de Maagd *et al.* (1996) *Appl. Environ. Microbiol.* 62:1537-1543; Ge *et al.* (1991) *J. Biol. Chem.* 266:17954-17958; Schnepf *et al.* (1990) *J. Biol. Chem.* 265:20923-20930; Rang *et al.* 91999) *Appl. Environ. Micriobiol.* 65:2918-2925).

Plant Transformation

Transformation of plant cells can be accomplished by one of several techniques known in the art. First, one engineers the delta-endotoxin or delta-endotoxin-associated gene in a way that allows its expression in plant cells. Typically a construct that expresses such a protein would contain a promoter to drive transcription of the gene, as well as a 3′ untranslated region to allow transcription termination and polyadenylation. The organization of such constructs is well known in the art. In some instances, it may be useful to engineer the gene such that the resulting peptide is secreted, or otherwise targeted within the plant cell. For example, the gene can be engineered to contain a signal peptide to facilitate transfer of the peptide to the endoplasmic reticulum. It may also be preferable to engineer the plant expression cassette to contain an intron, such that mRNA processing of the intron is required for expression.

Typically this 'plant expression cassette' will be inserted into a 'plant transformation vector'. This plant transformation vector may be comprised of one or more DNA vectors needed for achieving plant transformation. For example, it is a common practice in the art to utilize plant transformation vectors that are comprised of more than one contiguous DNA segment. These vectors are often referred to in the art as 'binary vectors'. Binary vectors as well as vectors with helper plasmids are most often used for *Agrobacterium*-mediated transformation, where the size and complexity of DNA segments needed to achieve efficient transformation is quite

large, and it is advantageous to separate functions onto separate DNA molecules. Binary vectors typically contain a plasmid vector that contains the cis-acting sequences required for T-DNA transfer (such as left border and right border), a selectable marker that is engineered to be capable of expression in a plant cell, and a 'gene of interest' (a gene engineered to be capable of expression in a plant cell for which generation of transgenic plants is desired). Also present on this plasmid vector are sequences required for bacterial replication. The cis-acting sequences are arranged in a fashion to allow efficient transfer into plant cells and expression therein. For example, the selectable marker gene and the gene of interest are located between the left and right borders. Often a second plasmid vector contains the trans-acting factors that mediate T-DNA transfer from *Agrobacterium* to plant cells. This plasmid often contains the virulence functions (Vir genes) that allow infection of plant cells by *Agrobacterium*, and transfer of DNA by cleavage at border sequences and vir-mediated DNA transfer, as in understood in the art (Hellens and Mullineaux (2000) *Trends in Plant Science*, 5:446-451). Several types of *Agrobacterium* strains (e.g. LBA4404, GV3101, EHA101, EHA105, etc.) can be used for plant transformation. The second plasmid vector is not necessary for transforming the plants by other methods such as microprojection, microinjection, electroporation, polyethelene glycol, etc.

In general, plant transformation methods involve transferring heterologous DNA into target plant cells (e.g. immature or mature embryos, suspension cultures, undifferentiated callus, protoplasts, etc.), followed by applying a maximum threshold level of appropriate selection (depending on the selectable marker gene) to recover the transformed plant cells from a group of untransformed cell mass. Explants are typically transferred to a fresh supply of the same medium and cultured routinely. Subsequently, the transformed cells are differentiated into shoots after placing on regeneration medium supplemented with a maximum threshold level of selecting agent. The shoots are then transferred to a selective rooting medium for recovering rooted shoot or plantlet. The transgenic plantlet then grows into a mature plant and produces fertile seeds (e.g. Hiei *et al.* (1994) *The Plant Journal* 6: 271-282; Ishida *et al.* (1996) *Nature Biotechnology* 14: 745-750). Explants are typically transferred to a fresh supply of the same medium and cultured routinely. A general description of the techniques and methods for generating transgenic plantlets are found in Ayres and

Park, 1994 (*Critical Reviews in Plant Science* 13: 219-239) and Bommineni and Jauhar, 1997 (*Maydica* 42: 107-120). Since the transformed material contains many cells; both transformed and non-transformed cells are present in any piece of subjected target callus or tissue or group of cells. The ability to kill non-transformed cells and allow transformed cells to proliferate results in transformed plant cultures. Often, the ability to remove non-transformed cells is a limitation to rapid recovery of transformed plant cells and successful generation of transgenic plants.

Generation of transgenic plants may be performed by one of several methods, including but not limited to introduction of heterologous DNA by *Agrobacterium* into plant cells (*Agrobacterium*-mediated transformation), bombardment of plant cells with heterologous foreign DNA adhered to particles, and various other non-particle direct-mediated methods (e.g. Hiei *et al.* (1994) *The Plant Journal* 6: 271-282; Ishida *et al.* (1996) *Nature Biotechnology* 14: 745-750; Ayres and Park (1994) *Critical Reviews in Plant Science* 13: 219-239; Bommineni and Jauhar (1997) *Maydica* 42: 107-120) to transfer DNA.

Transformation protocols as well as protocols for introducing nucleotide sequences into plants may vary depending on the type of plant or plant cell, i.e., monocot or dicot, targeted for transformation. Suitable methods of introducing nucleotide sequences into plant cells and subsequent insertion into the plant genome include microinjection (Crossway *et al.* (1986) *Biotechniques* 4:320-334), electroporation (Riggs *et al.* (1986) *Proc. Natl. Acad. Sci. USA* 83:5602-5606, *Agrobacterium*-mediated transformation (U.S. Patent No. 5,563,055; U.S. Patent No. 5,981,840), direct gene transfer (Paszkowski *et al.* (1984) *EMBO J.* 3:2717-2722), and ballistic particle acceleration (see, for example, U.S. Patent No. 4,945,050; U.S. Patent No. 5,879,918; U.S. Patent No. 5,886,244; U.S. Patent No. 5,932,782; Tomes *et al.* (1995) "Direct DNA Transfer into Intact Plant Cells via Microprojectile Bombardment," in *Plant Cell, Tissue, and Organ Culture: Fundamental Methods*, ed. Gamborg and Phillips (Springer-Verlag, Berlin); McCabe *et al.* (1988) *Biotechnology* 6:923-926); aerosol beam transformation (U.S. Published Application No. 20010026941; U.S. Patent No. 4,945,050; International Publication No. WO 91/00915; U.S. Published Application No. 2002015066); and Lec1 transformation (WO 00/28058). Also see Weissinger *et al.* (1988) *Ann. Rev. Genet.* 22:421-477; Sanford *et al.* (1987) *Particulate Science and Technology* 5:27-37; Christou *et al.*

(1988) *Plant Physiol.* 87:671-674; McCabe *et al.* (1988) *Bio/Technology* 6:923-926; Finer and McMullen (1991) *In Vitro Cell Dev. Biol.* 27P:175-182; Singh *et al.* (1998) *Theor. Appl. Genet.* 96:319-324 (soybean); Datta *et al.* (1990) *Biotechnology* 8:736-740; Klein *et al.* (1988) *Proc. Natl. Acad. Sci. USA* 85:4305-4309; U.S. Patent No. 5,240,855; U.S. Patent Nos. 5,322,783 and 5,324,646; Tomes *et al. (1995)* "Direct DNA Transfer into Intact Plant Cells via Microprojectile Bombardment," in *Plant Cell, Tissue, and Organ Culture: Fundamental Methods*, ed. Gamborg (Springer-Verlag, Berlin); Klein *et al.* (1988) *Plant Physiol.* 91:440-444; Hooykaas-Van Slogteren *et al.* (1984) *Nature (London)* 311:763-764; U.S. Patent No. 5,736,369; Bytebier *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84:5345-5349 (Liliaceae); De Wet *et al.* (1985) in *The Experimental Manipulation of Ovule Tissues,* ed. Chapman *et al.* (Longman, New York), pp. 197-209; Kaeppler *et al.* (1990) *Plant Cell Reports* 9:415-418 and Kaeppler *et al.* (1992) *Theor. Appl. Genet.* 84:560-566; D'Halluin *et al.* (1992) *Plant Cell* 4:1495-1505; Li *et al.* (1993) *Plant Cell Reports* 12:250-255 and Christou and Ford (1995) *Annals of Botany* 75:407-413; Osjoda *et al.* (1996) *Nature Biotechnology* 14:745-750; all of which are herein incorporated by reference.

Following integration of heterologous foreign DNA into plant cells, one then applies a maximum threshold level of appropriate selection in the medium to kill the untransformed cells and separate and proliferate the putatively transformed cells that survive from this selection treatment by transferring regularly to a fresh medium. By continuous passage and challenge with appropriate selection, one identifies and proliferates the cells that are transformed with the plasmid vector. Then molecular and biochemical methods will be used for confirming the presence of the integrated heterologous gene of interest in the genome of transgenic plant.

The cells that have been transformed may be grown into plants in accordance with conventional ways. See, for example, McCormick *et al.* (1986) *Plant Cell Reports* 5:81-84. These plants may then be grown, and either pollinated with the same transformed strain or different strains, and the resulting hybrid having constitutive expression of the desired phenotypic characteristic identified. Two or more generations may be grown to ensure that expression of the desired phenotypic characteristic is stably maintained and inherited and then seeds harvested to ensure expression of the desired phenotypic characteristic has been achieved. In this manner, the present invention provides transformed seed (also referred to as "transgenic seed")

having a nucleotide construct of the invention, for example, an expression cassette of the invention, stably incorporated into their genome.

The delta-endotoxin or delta-endotoxin-associated sequences of the invention may be provided in expression cassettes for expression in the plant of interest. The cassette will include 5' and 3' regulatory sequences operably linked to a sequence of the invention. By "operably linked" is intended a functional linkage between a promoter and a second sequence, wherein the promoter sequence initiates and mediates transcription of the DNA sequence corresponding to the second sequence. Generally, operably linked means that the nucleic acid sequences being linked are contiguous and, where necessary to join two protein coding regions, contiguous and in the same reading frame. The cassette may additionally contain at least one additional gene to be cotransformed into the organism. Alternatively, the additional gene(s) can be provided on multiple expression cassettes.

Such an expression cassette is provided with a plurality of restriction sites for insertion of the delta-endotoxin or delta-endotoxin-associated sequence to be under the transcriptional regulation of the regulatory regions.

The expression cassette will include in the 5'-3' direction of transcription, a transcriptional and translational initiation region (i.e., a promoter), a DNA sequence of the invention, and a transcriptional and translational termination region (i.e., termination region) functional in plants. The promoter may be native or analogous, or foreign or heterologous, to the plant host and/or to the DNA sequence of the invention. Additionally, the promoter may be the natural sequence or alternatively a synthetic sequence. Where the promoter is "native" or "homologous" to the plant host, it is intended that the promoter is found in the native plant into which the promoter is introduced. Where the promoter is "foreign" or "heterologous" to the DNA sequence of the invention, it is intended that the promoter is not the native or naturally occurring promoter for the operably linked DNA sequence of the invention.

The termination region may be native with the transcriptional initiation region, may be native with the operably-linked DNA sequence of interest, may be native with the plant host, or may be derived from another source (i.e., foreign or heterologous to the promoter, the DNA sequence of interest, the plant host, or any combination thereof). Convenient termination regions are available from the Ti-plasmid of *A. tumefaciens*, such as the octopine synthase and nopaline synthase termination regions.

See also Guerineau *et al.* (1991) *Mol. Gen. Genet.* 262:141-144; Proudfoot (1991) *Cell* 64:671-674; Sanfacon *et al.* (1991) *Genes Dev.* 5:141-149; Mogen *et al.* (1990) *Plant Cell* 2:1261-1272; Munroe *et al.* (1990) *Gene* 91:151-158; Ballas *et al.* (1989) *Nucleic Acids Res.* 17:7891-7903; and Joshi *et al.* (1987) *Nucleic Acid Res.* 15:9627-9639.

Where appropriate, the gene(s) may be optimized for increased expression in the transformed host cell. That is, the genes can be synthesized using host cell-preferred codons for improved expression, or may be synthesized using codons at a host-preferred codon usage frequency. See, for example, Campbell and Gowri (1990) *Plant Physiol.* 92:1-11 for a discussion of host-preferred codon usage. Methods are known in the art for synthesizing plant-preferred genes. See, for example, U.S. Patent Nos. 6,320,100; 6,075,185; 5,380,831; and 5,436,391, U.S. Published Application Nos. 20040005600 and 20010003849, and Murray *et al.* (1989) *Nucleic Acids Res.* 17:477-498, herein incorporated by reference.

In one embodiment, the nucleic acids of interest are targeted to the chloroplast for expression. In this manner, where the nucleic acid of interest is not directly inserted into the chloroplast, the expression cassette will additionally contain a nucleic acid encoding a transit peptide to direct the gene product of interest to the chloroplasts. Such transit peptides are known in the art. See, for example, Von Heijne *et al.* (1991) *Plant Mol. Biol. Rep.* 9:104-126; Clark *et al.* (1989) *J. Biol. Chem.* 264:17544-17550; Della-Cioppa *et al.* (1987) *Plant Physiol.* 84:965-968; Romer *et al.* (1993) *Biochem. Biophys. Res. Commun.* 196:1414-1421; and Shah *et al.* (1986) *Science* 233:478-481.

Methods for transformation of chloroplasts are known in the art. See, for example, Svab *et al.* (1990) *Proc. Natl. Acad. Sci. USA* 87:8526-8530; Svab and Maliga (1993) *Proc. Natl. Acad. Sci. USA* 90:913-917; Svab and Maliga (1993) *EMBO J.* 12:601-606. The method relies on particle gun delivery of DNA containing a selectable marker and targeting of the DNA to the plastid genome through homologous recombination. Additionally, plastid transformation can be accomplished by transactivation of a silent plastid-borne transgene by tissue-preferred expression of a nuclear-encoded and plastid-directed RNA polymerase. Such a system has been reported in McBride *et al.* (1994) *Proc. Natl. Acad. Sci. USA* 91:7301-7305.

The nucleic acids of interest to be targeted to the chloroplast may be optimized for expression in the chloroplast to account for differences in codon usage between the plant nucleus and this organelle. In this manner, the nucleic acids of interest may be synthesized using chloroplast-preferred codons. See, for example, U.S. Patent No. 5,380,831, herein incorporated by reference.

Evaluation of Plant Transformation

Following introduction of heterologous foreign DNA into plant cells, the transformation or integration of heterologous gene in the plant genome is confirmed by various methods such as analysis of nucleic acids, proteins and metabolites associated with the integrated gene.

PCR Analysis: PCR analysis is a rapid method to screen transformed cells, tissue or shoots for the presence of incorporated gene at the earlier stage before transplanting into the soil (Sambrook and Russell, 2001). PCR is carried out using oligonucleotide primers specific to the gene of interest or *Agrobacterium* vector background, etc.

Southern Analysis: Plant transformation is confirmed by Southern blot analysis of genomic DNA (Sambrook and Russell, 2001). In general, total DNA is extracted from the transformant, digested with appropriate restriction enzymes, fractionated in an agarose gel and transferred to a nitrocellulose or nylon membrane. The membrane or "blot" then is probed with, for example, radiolabeled ^{32}P target DNA fragment to confirm the integration of introduced gene in the plant genome according to standard techniques (Sambrook and Russell, 2001. *Molecular Cloning: A Laboratory Manual.* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY).

Northern Analysis: RNA is isolated from specific tissues of transformant, fractionated in a formaldehyde agarose gel, blotted onto a nylon filter according to standard procedures that are routinely used in the art (Sambrook, J., and Russell, D.W. 2001. *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY). Expression of RNA encoded by the delta-endotoxin or delta-endotoxin-associated is then tested by hybridizing the filter to a radioactive

probe derived from a delta-endotoxin or delta-endotoxin-associated protein , by methods known in the art (Sambrook and Russell, 2001).

Western blot and Biochemical assays: Western blot and biochemical assays and the like may be carried out on the transgenic plants to confirm the presence of protein encoded by the delta-endotoxin or delta-endotoxin-associated gene by standard procedures (Sambrook, J., and Russell, D.W. 2001. *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY) using antibodies that bind to one or more epitopes present on the delta-endotoxin or delta-endotoxin-associated protein.

Pesticidal activity in plants

In another aspect of the invention, one may generate transgenic plants expressing delta-endotoxin or delta-endotoxin-associated proteins that have pesticidal activity. Methods described above by way of example may be utilized to generate transgenic plants, but the manner in which the transgenic plant cells are generated is not critical to this invention. Methods known or described in the art such as *Agrobacterium*-mediated transformation, aerosol beam, biolistic transformation, and non-particle-mediated methods may be used at the discretion of the experimenter. Plants expressing delta-endotoxin or delta-endotoxin-associated proteins may be isolated by common methods described in the art, for example by transformation of callus, selection of transformed callus, and regeneration of fertile plants from such transgenic callus. In such process, one may use any gene as a selectable marker so long as its expression in plant cells confers ability to identify or select for transformed cells.

A number of markers have been developed for use with plant cells, such as resistance to chloramphenicol, the aminoglycoside G418, hygromycin, or the like. Other genes that encode a product involved in chloroplast metabolism may also be used as selectable markers. For example, genes that provide resistance to plant herbicides such as glyphosate, bromoxynil, or imidazolinone may find particular use. Such genes have been reported (Stalker *et al.* (1985) *J. Biol. Chem.* 263:6310-6314 (bromoxynil resistance nitrilase gene); and Sathasivan *et al.* (1990) *Nucl. Acids Res.* 18:2188 (AHAS imidazolinone resistance gene).

Fertile plants expressing a delta-endotoxin or a delta-endotoxin-associated protein may be tested for pesticidal activity, and the plants showing optimal activity selected for further breeding. Methods are available in the art to assay for pest activity. Generally, the protein is mixed and used in feeding assays. See, for example Marrone *et al.* (1985) *J. of Economic Entomology* 78:290-293.

Use in Pesticidal Control

General methods for employing the strains of the invention in pesticide control or in engineering other organisms as pesticidal agents are known in the art. See, for example U.S. Patent No. 5,039,523 and EP 0480762A2.

The *Bacillus* strains of the invention or the microorganisms which have been genetically altered to contain the pesticidal gene and protein may be used for protecting agricultural crops and products from pests. In one aspect of the invention, whole, i.e., unlysed, cells of a toxin (pesticide)-producing organism are treated with reagents that prolong the activity of the toxin produced in the cell when the cell is applied to the environment of target pest(s).

Alternatively, the pesticide is produced by introducing a heterologous gene into a cellular host. Expression of the heterologous gene results, directly or indirectly, in the intracellular production and maintenance of the pesticide. In one aspect of this invention, these cells are then treated under conditions that prolong the activity of the toxin produced in the cell when the cell is applied to the environment of target pest(s). The resulting product retains the toxicity of the toxin. These naturally encapsulated pesticides may then be formulated in accordance with conventional techniques for application to the environment hosting a target pest, e.g., soil, water, and foliage of plants. See, for example EPA 0192319, and the references cited therein. Alternatively, one may formulate the cells expressing the genes of this invention such as to allow application of the resulting material as a pesticide.

The active ingredients of the present invention are normally applied in the form of compositions and can be applied to the crop area or plant to be treated, simultaneously or in succession, with other compounds. These compounds can be fertilizers, weed killers, cryoprotectants, surfactants, detergents, pesticidal soaps, dormant oils, polymers, and/or time-release or biodegradable carrier formulations that permit long-term dosing of a target area following a single application of the

formulation. They can also be selective herbicides, chemical insecticides, virucides, microbicides, amoebicides, pesticides, fungicides, bacteriocides, nematocides, mollusocides or mixtures of several of these preparations, if desired, together with further agriculturally acceptable carriers, surfactants or application-promoting adjuvants customarily employed in the art of formulation. Suitable carriers and adjuvants can be solid or liquid and correspond to the substances ordinarily employed in formulation technology, e.g. natural or regenerated mineral substances, solvents, dispersants, wetting agents, tackifiers, binders or fertilizers. Likewise the formulations may be prepared into edible "baits" or fashioned into pest "traps" to permit feeding or ingestion by a target pest of the pesticidal formulation.

Preferred methods of applying an active ingredient of the present invention or an agrochemical composition of the present invention which contains at least one of the pesticidal proteins produced by the bacterial strains of the present invention are leaf application, seed coating and soil application. The number of applications and the rate of application depend on the intensity of infestation by the corresponding pest.

The composition may be formulated as a powder, dust, pellet, granule, spray, emulsion, colloid, solution, or such like, and may be preparable by such conventional means as desiccation, lyophilization, homogenation, extraction, filtration, centrifugation, sedimentation, or concentration of a culture of cells comprising the polypeptide. In all such compositions that contain at least one such pesticidal polypeptide, the polypeptide may be present in a concentration of from about 1% to about 99% by weight.

Lepidopteran or coleopteran pests may be killed or reduced in numbers in a given area by the methods of the invention, or may be prophylactically applied to an environmental area to prevent infestation by a susceptible pest. Preferably the pest ingests, or is contacted with, a pesticidally-effective amount of the polypeptide. By "pesticidally-effective amount" is intended an amount of the pesticide that is able to bring about death to at least one pest, or to noticeably reduce pest growth, feeding, or normal physiological development. This amount will vary depending on such factors as, for example, the specific target pests to be controlled, the specific environment, location, plant, crop, or agricultural site to be treated, the environmental conditions, and the method, rate, concentration, stability, and quantity of application of the

pesticidally-effective polypeptide composition. The formulations may also vary with respect to climatic conditions, environmental considerations, and/or frequency of application and/or severity of pest infestation.

The pesticide compositions described may be made by formulating either the bacterial cell, crystal and/or spore suspension, or isolated protein component with the desired agriculturally-acceptable carrier. The compositions may be formulated prior to administration in an appropriate means such as lyophilized, freeze-dried, desiccated, or in an aqueous carrier, medium or suitable diluent, such as saline or other buffer. The formulated compositions may be in the form of a dust or granular material, or a suspension in oil (vegetable or mineral), or water or oil/water emulsions, or as a wettable powder, or in combination with any other carrier material suitable for agricultural application. Suitable agricultural carriers can be solid or liquid and are well known in the art. The term "agriculturally-acceptable carrier" covers all adjuvants, inert components, dispersants, surfactants, tackifiers, binders, etc. that are ordinarily used in pesticide formulation technology; these are well known to those skilled in pesticide formulation. The formulations may be mixed with one or more solid or liquid adjuvants and prepared by various means, e.g., by homogeneously mixing, blending and/or grinding the pesticidal composition with suitable adjuvants using conventional formulation techniques. Suitable formulations and application methods are described in U.S. Patent No. 6,468,523, herein incorporated by reference.

"Pest" includes but is not limited to, insects, fungi, bacteria, nematodes, mites, ticks, and the like. Insect pests include insects selected from the orders Coleoptera, Diptera, Hymenoptera, Lepidoptera, Mallophaga, Homoptera, Hemiptera, Orthroptera, Thysanoptera, Dermaptera, Isoptera, Anoplura, Siphonaptera, Trichoptera, etc., particularly Coleoptera, Lepidoptera, and Diptera.

Insect pests include insects selected from the orders Coleoptera, Diptera, Hymenoptera, Lepidoptera, Mallophaga, Homoptera, Hemiptera, Orthoptera, Thysanoptera, Dermaptera, Isoptera, Anoplura, Siphonaptera, Trichoptera, etc., particularly Coleoptera and Lepidoptera. Insect pests of the invention for the major crops include: Maize: *Ostrinia nubilalis*, European corn borer; *Agrotis ipsilon*, black cutworm; *Helicoverpa zea*, corn earworm; *Spodoptera frugiperda*, fall armyworm; *Diatraea grandiosella*, southwestern corn borer; *Elasmopalpus lignosellus*, lesser cornstalk borer; *Diatraea saccharalis*, surgarcane borer; *Diabrotica virgifera*, western

corn rootworm; *Diabrotica longicornis barberi*, northern corn rootworm; *Diabrotica undecimpunctata howardi*, southern corn rootworm; *Melanotus* spp., wireworms; *Cyclocephala borealis*, northern masked chafer (white grub); *Cyclocephala immaculata*, southern masked chafer (white grub); *Popillia japonica*, Japanese beetle; *Chaetocnema pulicaria*, corn flea beetle; *Sphenophorus maidis*, maize billbug; *Rhopalosiphum maidis*, corn leaf aphid; *Anuraphis maidiradicis*, corn root aphid; *Blissus leucopterus leucopterus*, chinch bug; *Melanoplus femurrubrum*, redlegged grasshopper; *Melanoplus sanguinipes*, migratory grasshopper; *Hylemya platura*, seedcorn maggot; *Agromyza parvicornis*, corn blot leafminer; *Anaphothrips obscrurus*, grass thrips; *Solenopsis milesta*, thief ant; *Tetranychus urticae*, twospotted spider mite; Sorghum: *Chilo partellus*, sorghum borer; *Spodoptera frugiperda*, fall armyworm; *Helicoverpa zea*, corn earworm; *Elasmopalpus lignosellus*, lesser cornstalk borer; *Feltia subterranea*, granulate cutworm; *Phyllophaga crinita*, white grub; *Eleodes, Conoderus*, and *Aeolus* spp., wireworms; *Oulema melanopus*, cereal leaf beetle; *Chaetocnema pulicaria*, corn flea beetle; *Sphenophorus maidis*, maize billbug; *Rhopalosiphum maidis*; corn leaf aphid; *Sipha flava*, yellow sugarcane aphid; *Blissus leucopterus leucopterus*, chinch bug; *Contarinia sorghicola*, sorghum midge; *Tetranychus cinnabarinus*, carmine spider mite; *Tetranychus urticae*, twospotted spider mite; Wheat: *Pseudaletia unipunctata*, army worm; *Spodoptera frugiperda*, fall armyworm; *Elasmopalpus lignosellus*, lesser cornstalk borer; *Agrotis orthogonia*, western cutworm; *Elasmopalpus lignosellus*, lesser cornstalk borer; *Oulema melanopus*, cereal leaf beetle; *Hypera punctata*, clover leaf weevil; *Diabrotica undecimpunctata howardi*, southern corn rootworm; Russian wheat aphid; *Schizaphis graminum*, greenbug; *Macrosiphum avenae*, English grain aphid; *Melanoplus femurrubrum*, redlegged grasshopper; *Melanoplus differentialis*, differential grasshopper; *Melanoplus sanguinipes*, migratory grasshopper; *Mayetiola destructor*, Hessian fly; *Sitodiplosis mosellana*, wheat midge; *Meromyza americana*, wheat stem maggot; *Hylemya coarctata*, wheat bulb fly; *Frankliniella fusca*, tobacco thrips; *Cephus cinctus*, wheat stem sawfly; *Aceria tulipae*, wheat curl mite; Sunflower: *Suleima helianthana*, sunflower bud moth; *Homoeosoma electellum*, sunflower moth; *zygogramma exclamationis*, sunflower beetle; *Bothyrus gibbosus*, carrot beetle; *Neolasioptera murtfeldtiana*, sunflower seed midge; Cotton: *Heliothis virescens*, cotton budworm; *Helicoverpa zea*, cotton bollworm; *Spodoptera exigua*, beet

armyworm; *Pectinophora gossypiella*, pink bollworm; *Anthonomus grandis*, boll weevil; *Aphis gossypii*, cotton aphid; *Pseudatomoscelis seriatus*, cotton fleahopper; *Trialeurodes abutilonea*, bandedwinged whitefly; *Lygus lineolaris*, tarnished plant bug; *Melanoplus femurrubrum*, redlegged grasshopper; *Melanoplus differentialis*, differential grasshopper; *Thrips tabaci*, onion thrips; *Franklinkiella fusca*, tobacco thrips; *Tetranychus cinnabarinus*, carmine spider mite; *Tetranychus urticae*, twospotted spider mite; Rice: *Diatraea saccharalis*, sugarcane borer; *Spodoptera frugiperda*, fall armyworm; *Helicoverpa zea*, corn earworm; *Colaspis brunnea*, grape colaspis; *Lissorhoptrus oryzophilus*, rice water weevil; *Sitophilus oryzae*, rice weevil; *Nephotettix nigropictus*, rice leafhopper; *Blissus leucopterus leucopterus*, chinch bug; *Acrosternum hilare*, green stink bug; Soybean: *Pseudoplusia includens*, soybean looper; *Anticarsia gemmatalis*, velvetbean caterpillar; *Plathypena scabra*, green cloverworm; *Ostrinia nubilalis*, European corn borer; *Agrotis ipsilon*, black cutworm; *Spodoptera exigua*, beet armyworm; *Heliothis virescens*, cotton budworm; *Helicoverpa zea*, cotton bollworm; *Epilachna varivestis*, Mexican bean beetle; *Myzus persicae*, green peach aphid; *Empoasca fabae*, potato leafhopper; *Acrosternum hilare*, green stink bug; *Melanoplus femurrubrum*, redlegged grasshopper; *Melanoplus differentialis*, differential grasshopper; *Hylemya platura*, seedcorn maggot; *Sericothrips variabilis*, soybean thrips; *Thrips tabaci*, onion thrips; *Tetranychus turkestani*, strawberry spider mite; *Tetranychus urticae*, twospotted spider mite; Barley: *Ostrinia nubilalis*, European corn borer; *Agrotis ipsilon*, black cutworm; *Schizaphis graminum*, greenbug; *Blissus leucopterus leucopterus*, chinch bug; *Acrosternum hilare*, green stink bug; *Euschistus servus*, brown stink bug; *Delia platura*, seedcorn maggot; *Mayetiola destructor*, Hessian fly; *Petrobia latens*, brown wheat mite; Oil Seed Rape: *Brevicoryne brassicae*, cabbage aphid; *Phyllotreta cruciferae*, Flea beetle; *Mamestra configurata*, Bertha armyworm; *Plutella xylostella*, Diamond-back moth; *Delia* ssp., Root maggots.

Nematodes include parasitic nematodes such as root-knot, cyst, and lesion nematodes, including *Heterodera* spp., *Meloidogyne* spp., and *Globodera* spp.; particularly members of the cyst nematodes, including, but not limited to, *Heterodera glycines* (soybean cyst nematode); *Heterodera schachtii* (beet cyst nematode); *Heterodera avenae* (cereal cyst nematode); and *Globodera rostochiensis* and

Globodera pailida (potato cyst nematodes). Lesion nematodes include *Pratylenchus* spp.

The following examples are offered by way of illustration and not by way of limitation.

EXPERIMENTAL

Example 1. Extraction of Plasmid DNA

Plasmid DNA from strains ATX 13026 or ATX 13002 were prepared in the following way. A pure culture of strain ATX13026 or strain ATX13002 was grown in large quantities of rich media. The culture was centrifuged to harvest the cell pellet. The cell pellet was then prepared by treatment with SDS by methods known in the art, resulting in breakage of the cell wall and release of DNA. Proteins and large genomic DNA was then precipitated by a high salt concentration. The plasmid DNA was precipitated by standard ethanol precipitation. The plasmid DNA was separated from any remaining chromosomal DNA by high-speed centrifugation through a cesium chloride gradient. The DNA was visualized in the gradient by UV light and the band of lower density (i.e. the lower band) was extracted using a syringe. This band contained the plasmid DNA from the strain (either ATX 13026 or ATX 13002) The quality of the DNA was checked by visualization on an agarose gel by methods known in the art.

Example 2. Cloning of Genes

The purified plasmid DNA was sheared into 5-10 kb sized fragments and the 5′ and 3′ single stranded overhangs repaired using T4 DNA polymerase and Klenow fragment in the presence of all four dNTPs, as known in the art. Phosphates were then attached to the 5′ ends by treatment with T4 polynucleotide kinase, as known in the art. The repaired DNA fragments were ligated overnight into a standard high copy vector (i.e. pBluescript SK+), suitably prepared to accept the inserts as known in the art (for example by digestion with a restriction enzyme producing blunt ends).

The quality of the library was analyzed by digesting a subset of clones with a restriction enzyme known to have a cleavage site flanking the cloning site. A high percentage of clones were determined to contain inserts, with an average insert size of 5-6 kb.

Example 3. High Throughput Sequencing of Library Plates

The libraries prepared by the methods above were plated onto rich media containing the appropriate antibiotic to maintain the plasmids clones, and colonies were individually picked into 96-well blocks containing 2 mls of media containing the appropriate antibiotic. These blocks were grown overnight at 37°C at a shaking speed of 350 rpm. The blocks were centrifuged to harvest the cells to the bottom of the block. Plasmid DNA was isolated from these cultures by standard alkaline lysis prep in a high throughput format.

The end sequences of clones from this library were determined for a large number of clones from each block in the following way: The DNA sequence of each clone chosen for analysis was determined using the fluorescent dye terminator sequencing technique (Applied Biosystems) and standard primers flanking each side of the cloning site. Once the reactions had been carried out in the thermocycler, the DNA was precipitated using standard ethanol precipitation. The DNA was resuspended in water and loaded onto a capillary sequencing machine. Each library plate of DNA was sequenced from either end of the cloning site, yielding two reads per plate over each insert.

Example 4. Assembly and Screening of Sequencing Data

DNA sequences obtained were compiled into an assembly project and aligned together to form contigs. This can be done efficiently using a computer program, such as Vector NTi, or alternatively by using the Pred/Phrap suite of DNA alignment and analysis programs. These contigs, along with any individual read that may not have been added to a contig, were compared to a compiled database of all classes of known pesticidal genes. Contigs or individual reads identified as having identity to a known endotoxin or pesticidal gene were analyzed further. Among the sequences obtained, clones pAX004, pAX006, pAX007, pAX008, pAX009, and pAX014 contained DNA identified as having homology to known endotoxin genes. Therefore, these clones were selected for further sequencing.

Example 5. Sequencing and Identification of Delta-Endotoxin Genes

Primers were designed to anneal to sequences with homology to endotoxin genes, in a manner such that DNA sequences generated from such primers would overlap existing DNA sequence of the clone(s). This process, known as "oligo walking," is well known in the art. This process was utilized to determine the entire DNA sequence of the region exhibiting homology to a known endotoxin gene. In the case of the clones mentioned above, this process was used to determine the DNA sequence of the entire clone, resulting in a single nucleotide sequence for each gene. The completed DNA sequence was then placed back into the original large assembly for further validation. This allowed incorporation of more DNA sequence reads into the contig, resulting in multiple reads of coverage over the entire region.

Analysis of the DNA sequence of each region with homology to a known endotoxin gene identified an open reading frame with homology to a known delta-endotoxin gene. The open reading frame identified from pAX004 is designated as AXMI-004. The open reading frame identified from pAX006 is designated AXMI-006. The open reading frame identified from pAX007 is designated AXMI-007. The open reading frame identified from pAX008 is designated AXMI-008. The open reading frame identified from pAX009 is designated AXMI-009. The open reading frame identified from pAX014 is designated AXMI-014. The DNA sequence of AXMI-004 is provided as SEQ ID NOS:1 and 2, and the amino acid sequence of the predicted AMXI-004 protein is provided as SEQ ID NO:3. An alternate start site for AXMI-004 at nucleotide 385 of SEQ ID NO:1 generates the amino acid sequence provided as SEQ ID NO:5. The DNA sequence of AXMI-006 is provided as SEQ ID NO:6, and the amino acid sequence of the predicted AMXI-006 protein is provided in SEQ ID NO:7. The DNA sequence of AXMI-007 is provided as SEQ ID NO:8, and the amino acid sequence of the predicted AMXI-007 protein is provided in SEQ ID NO:9. An alternate start site for AXMI-007 at nucleotide 151 of SEQ ID NO:8 generates the amino acid sequence provided as SEQ ID NO:11. The DNA sequence of AXMI-008 is provided as SEQ ID NOS:12 and 13, and the amino acid sequence of the predicted AMXI-008 protein is provided in SEQ ID NO:14. An alternate start site for AXMI-008 at nucleotide 177 of SEQ ID NO:12 generates the amino acid sequence provided as SEQ ID NO:16. Further analysis identified an open reading frame immediately 3' to the end of the AXMI-008 open reading frame. This predicted

amino acid sequence of this orf, referred to herein as AXMI-008orf2, is provided in SEQ ID NO:18. The DNA sequence of AXMI-009 is provided as SEQ ID NO:19, and the amino acid sequence of the predicted AMXI-009 protein is provided in SEQ ID NO:20. An alternate start site for AXMI-009 at nucleotide 34 of SEQ ID NO:19 generates the amino acid sequence provided as SEQ ID NO:22. Another alternate start site for AXMI-009 at nucleotide 64 of SEQ ID NO:19 generates the amino acid sequence provided as SEQ ID NO:24. The DNA sequence of AXMI-014 is provided as SEQ ID NOS:25 and 26, and the amino acid sequence of the predicted AMXI-008 protein is provided as SEQ ID NO:27. An alternate start site for AXMI-014 at nucleotide 136 of SEQ ID NO:25 generates the amino acid sequence provided as SEQ ID NO:29.

Example 6. Homology of Isolated Genes to Known Endotoxin Genes

Searches of DNA and protein databases with the DNA sequences and amino acid sequences of the present invention reveal that these sequences are homologous to known endotoxins.

AXMI-004

Figure 1 shows an alignment of AXMI-004 with several endotoxins. Blast searches identify cry1Ca as having the strongest block of homology, with an overall sequence identity in the toxic domain of 43% (see Table 1).

Table 1. Amino Acid Identity of AXMI-004 with Exemplary Endotoxin Classes

Endotoxin	Percent Amino Acid Identity to AXMI-004	Percent Amino Acid Identity in Toxic Domains
cry1Ac*	17%	30%
cry1Ca*	24%	43%
cry2Aa	12%	12%
cry3Aa	33%	33%
cry1Ia	35%	37%
cry7Aa	19%	31%

AXMI-006

Figure 2 shows an alignment of AXMI-006 with several endotoxins. Blast searches identify cry4Aa as having the strongest block of homology, though alignment of AMXI-006 protein (SEQ ID NO:7) to a large set of endotoxin proteins shows that the most homologous protein is cry10Aa. The overall amino acid identity of cry10Aa to AXMI-006 is 25% (see Table 2). Inspection of the amino acid sequence of AXMI-006 suggests that it does not contain a C-terminal non-toxic domain as is present in several endotoxin families. By removing this C-terminal protein of the toxins from the alignment, the alignment reflects the amino acid identity present solely in the toxin domains (see Table 2, column three). This 'trimmed' alignment is shown in Figure 2.

Table 2. Amino Acid Identity of AXMI-006 with Exemplary Endotoxin Classes

Endotoxin	Percent Amino Acid Identity to AXMI-006	Percent Amino Acid Identity of truncated Toxins to AXMI-006
cry1Aa	11%	17%
cry1Ac	12%	19%
cry1Ia	20%	19%
cry3Aa	20%	19%
cry3Bb	22%	21%
cry4Aa	16%	26%
cry6Aa	5%	4%
cry7Aa	12%	19%
cry8Aa	13%	21%
cry10Aa	25%	25%
cry16Aa	23%	23%
cry19Ba	24%	24%
cry24Aa	19%	20%

AXMI-007

Blast searches identify *cry4Aa* as having the strongest block of homology to AXMI-007, though alignment of AMXI-007 protein (SEQ ID NO:9) to a large set of endotoxin proteins shows that the most homologous protein is *cry10Aa*. The overall

amino acid identity of *cry10Aa* to AXMI-007 is 25% (see Table 3). Inspection of the amino acid sequence of AXMI-007 suggests that it does not contain a C-terminal non-toxic domain as is present in several endotoxin families. By removing this C-terminal protein of the toxins from the alignment, the alignment reflects the amino acid identify present solely in the toxin domains (see Table 3, column three). This 'trimmed' alignment is shown in Figure 3.

Table 3. Amino Acid Identity of AXMI-007 with Exemplary Endotoxin Classes

Endotoxin	Percent Amino Acid Identity to AXMI-007	Percent Amino Acid Identity of truncated Toxins to AXMI-007
cry1Aa	11%	17%
cry1Ac	12%	20%
cry1Ia	19%	18%
cry3Aa	19%	19%
cry3Bb	21%	21%
cry4Aa	17%	27%
cry6Aa	5%	4%
cry7Aa	13%	19%
cry8Aa	13%	20%
cry10Aa	25%	25%
cry16Aa	24%	24%
cry19Ba	25%	25%
cry24Aa	19%	19%

AXMI-008

Blast searches identify *cry40Aa* as having the strongest block of homology to AXMI-008, and alignment of AMXI-008 protein (SEQ ID NO:14) to a large set of endotoxin proteins shows that the most homologous protein is cry40Aa. The overall amino acid identity of *cry40Aa* to AXMI-008 is 66% (see Table 4). Inspection of the amino acid sequence of AXMI-008 suggests that it does not contain a C-terminal non-toxic domain as is present in several endotoxin families. By removing this C-terminal protein of the toxins from the alignment, the alignment reflects the amino acid

identify present solely in the toxin domains (see Table 4, column three). This 'trimmed' alignment is shown in Figure 4.

Table 4. Amino Acid Identity of AXMI-008 with Exemplary Endotoxin Classes

Endotoxin	Percent Amino Acid Identity to AXMI-008	Percent Amino Acid Identity of truncated Toxins to AXMI-008
cry1Aa	11%	20%
cry1Ac	11%	20%
cry1Ia	22%	22%
cry2A	10%	10%
cry3Aa	21%	21%
cry3Bb	21%	21%
cry4Aa	13%	21%
cry4Ba	13%	20%
cry6Aa	5%	5%
cry7Aa	12%	20%
cry8Aa	13%	22%
cry10Aa	20%	20%
cry16Aa	22%	22%
cry19Ba	21%	22%
cry24Aa	26%	26%
cry25Aa	23%	23%
cry39Aa	25%	25%
cry40Aa	66%	66%

The open reading frame immediately downstream (3') to the AXMI-008 coding region has homology to known endotoxin-related proteins. Blast searches identify *crybun3orf2* (the downstream orf of *cry40Aa*) as having the strongest block of homology. Several other orf-2 like proteins are present in databases, and an alignment of AMXI-008-orf2 protein (SEQ ID NO:18) to a set of these proteins is shown in Figure 5. These proteins also share homology to the C-terminal non-toxic

domain of *cry4Aa* and *cry4Ba*. The overall amino acid identity of AXMI-8-orf2 to *cry40Aaorf2* is 86% (see Table 5).

Table 5. Amino acid identity of AXMI-008-orf2 to related proteins

Protein	Percent amino acid identity to AXMI-008-orf2
crybun3orf2 (*cry40Aa orf2*)	86%
crybun2orf2 (*cry39Aa orf2*)	85%
cry19Aorf2	62%
C-terminus *cry4Aa*	53%
C-terminus *cry4Ba*	54%

AXMI-009

Blast searches identify cryBAa as having the strongest block of homology to AXMI-009, and alignment of AMXI-009 protein (SEQ ID NO:20) to a large set of endotoxin proteins shows that the most homologous proteins are cry3Ba and cry16Aa. The overall amino acid identity of cry3Ba and cry16Aa to AXMI-009 is 26% (see Table 6). Inspection of the amino acid sequence of AXMI-009 suggests that it does not contain a C-terminal non-toxic domain as is present in several endotoxin families. By removing this C-terminal protein of the toxins from the alignment, the alignment reflects the amino acid identify present solely in the toxin domains (see Table 6, column three). This 'trimmed' alignment is shown in Figure 6.

Table 6. Amino Acid Identity of AXMI-009 with Exemplary Endotoxin Classes

Endotoxin	Percent Amino Acid Identity to AXMI-009	Percent Amino Acid Identity of truncated Toxins to AXMI-009
cry1Aa	12%	20%
cry1Ac	13%	23%
cry1Ca	13%	24
cry1Ia	24%	26%
cry3Aa	24%	25%
cry3Ba	26%	27%
cry3Bb	25%	27%
cry4Aa	13%	24%
cry6Aa	7%	5%
cry7Aa	15%	25%
cry8Aa	17%	28%%
cry10Aa	24%	24%
cry16Aa	26%	26%
cry19Ba	24%	25%
cry24Aa	25%	27%
cry25Aa	23%	23%
cry40Aa	19%	24%

AXMI-014

Blast searches identify *cry40Aa* as having the strongest block of homology to AXMI-014, and alignment of AMXI-0014 protein (SEQ ID NO:27) to a large set of endotoxin proteins shows that the most homologous protein is cry40Aa. The overall amino acid identity of *cry40Aa* to AXMI-014 is 55% (see Table 7). Inspection of the amino acid sequence of AXMI-014 suggests that it does not contain a C-terminal non-toxic domain as is present in several endotoxin families. By removing this C-terminal protein of the toxins from the alignment, the alignment reflects the amino acid identify present solely in the toxin domains (see Table 7, column three). This 'trimmed' alignment is shown in Figure 7.

Table 7. Amino Acid Identity of AXMI-014 with Exemplary Endotoxin Classes

Endotoxin	Percent Amino Acid Identity to AXMI-014	Percent Amino Acid Identity of truncated Toxins to AXMI-014
cry1Aa	12%	21%
cry1Ac	12%	22%
cry1Ia	20%	21%
cry2A	12%	12%
cry3Aa	20%	20%
cry3Bb	22%	22%
cry4Aa	12%	19%
cry4Ba	11%	19%
cry6Aa	6%	6%
cry7Aa	13%	21%
cry8Aa	14%	22%
cry10Aa	22%	22%
cry16Aa	24%	24%
cry19Ba	24%	24%
cry24Aa	29%	29%
cry25Aa	23%	23%
cry39Aa	22%	22%
cry40Aa	55%	55%

Example 7. Homology between AXMI-006 and AXMI-007

Comparison of the amino acid sequences of AXMI-007 with AXMI-006 shows that the two toxins share significant amino acid homology. Alignment of the amino acid sequence of AXMI-006 (SEQ ID NO:7) and AXMI-007 (SEQ ID NO:9) show the proteins to be 85 % identical at the amino acid level. Thus AXMI-006 and AXMI-007 constitute a new class of related endotoxins.

Example 8. Assays for Pesticidal Activity

The ability of a pesticidal protein to act as a pesticide upon a pest is often assessed in a number of ways. One way well known in the art is to perform a feeding assay. In such a feeding assay, one exposes the pest to a sample containing either compounds to be tested, or control samples. Often this is performed by placing the material to be tested, or a suitable dilution of such material, onto a material that the pest will ingest, such as an artificial diet. The material to be tested may be composed of a liquid, solid, or slurry. The material to be tested may be placed upon the surface and then allowed to dry. Alternatively, the material to be tested may be mixed with a molten artificial diet, then dispensed into the assay chamber. The assay chamber may be, for example, a cup, a dish, or a well of a microtiter plate.

Assays for sucking pests (for example aphids) may involve separating the test material from the insect by a partition, ideally a portion that can be pierced by the sucking mouthparts of the sucking insect, to allow ingestion of the test material. Often the test material is mixed with a feeding stimulant, such as sucrose, to promote ingestion of the test compound.

Other types of assays can include microinjection of the test material into the mouth, or gut of the pest, as well as development of transgenic plants, followed by test of the ability of the pest to feed upon the transgenic plant. Plant testing may involve isolation of the plant parts normally consumed, for example, small cages attached to a leaf, or isolation of entire plants in cages containing insects.

Other methods and approaches to assay pests are known in the art, and can be found, for example in Robertson, J. L. & H. K. Preisler. 1992. *Pesticide bioassays with arthropods*. CRC, Boca Raton, FL. Alternatively, assays are commonly described in
the journals "Arthropod Management Tests" and "Journal of Economic Entomology" or by discussion with members of the Entomological Society of America (ESA).

Example 9. Cloning of AXMI-006 for Protein Expression

AXMI-006 was cloned into a vector for *E. coli* expression as follows. pAX480 contains the kanamycin resistance gene for selection of transformants, and the *tac* promoter which is inducible by IPTG for regulated protein expression. pAX480 was modified by inserting a DNA segment encoding a 6xHis-tag region

immediately upstream of the insert cloning region, such that resulting clones contain a 6xHis-tag at the N-terminus of the expressed protein. Methods for expressing proteins with 6xHis-tag fusions, and their use for purification and analysis of protein expression are well known in the art.

The coding sequence for AXMI-006 was PCR-amplified using *PfuUltra*™ High-Fidelity DNA Polymerase (Stratagene). Oligonucleotide primers were designed such that the resulting PCR product contained desired restriction sites near each end, to facilitate cloning. The resulting PCR product (approximately 2.2 kb) was digested with the appropriate restriction enzyme, and subcloned into the modified pAX480. Insert-containing clones were identified by restriction analysis. The resulting clone, pAX906, contained the AXMI-006 open reading frame fused to the six his tag, such that transcription and translation resulted in production of a 'fusion protein' with a stretch of six histidines. The DNA sequence of pAX906 was confirmed by DNA sequence analysis and subsequently transformed into chemically competent *E. coli* BL21, as described by the manufacturer (Stratagene, La Jolla, CA).

A single colony of pAX906 in BL21 was inoculated into LB media supplemented with kanamycin and grown for several hours at 37°C with vigorous agitation. These cultures were grown to an OD_{600} ranging from 0.6-0.8; then protein production was induced by addition of 0.1 mM IPTG. Cultures were grown under inducing conditions for 3 hours, and then the cells were pelleted by centrifugation and resuspended in PBS. Cells were sonicated using a Misonix Sonicator 3000 for a total of 30 seconds using 10-second sonication intervals and incubation on ice for one minute.

Example 10. Bioassay of AXMI-006 Activity on *Heliothis virescens* and *Spodoptera frugiperda*

Bioassays of sonicated pAX906 cultures were performed using artificial diet (Multiple Species Diet, Southland Products, Lake Village, Arkansas). Bioassays were carried out by applying sonicated pAX906 cells, or cells of the *E.coli* strain as a control, to the diet surface and allowing the diet surface to dry. Bioassays were performed in 24-well tissue culture plates. The bioassays were held in the dark at 25° C and 65% relative humidity. Trays were sealed with Breathe Easy Sealing Tape (Diversified Biotech, Boston, MA). Results were recorded at 5 days.

Table 8. Bioassay of AXMI-006 on *Spodoptera frugiperda*

Sample	Bioassay Result
AXMI-006	Stunting
Negative control	No Stunting

Table 9. Bioassay of AXMI-006 on *Heliothis virescens*

Sample	Bioassay Result
AXMI-006	Stunting
Negative Control	No Stunting

Stunting is defined reduced insect size, and severally reduced larval feeding. Stunted insects may also demonstrate avoidance of the treated diet compared to the untreated diet.

Example 11. Pesticidal Activity of AXMI-008, AXMI-009, and AXMI-014 on *Trichoplusia ni* (Cabbage Looper)

Escherichia coli strains containing either pAX008, pAX009 or pAX-014, as well as a culture of untransformed *Escherichia coli* were grown in 2 ml of LB Broth (Luria-Bertani Broth, Becton Dickinson & Company, Sparks, Md.) for 24 hours at 37° C with agitation at 250 rpm. Plasmid-containing strains were grown in grown in LB containing the appropriate antibiotic to select for maintenance of the plasmid in *E. coli*.

Bioassays were performed using artificial diet (Multiple Species Diet, Southland Products, Lake Village, Arkansas) in 24 well tissue culture plates. Bioassays were carried out by applying the *Escherichia coli* culture containing pAX-014 to the diet surface and allowing the diet surface to dry. The strains were applied as whole cultures to the diet at a concentration of 40 µl of culture per well. The bioassays were held in the dark at 25° C and 65% relative humidity. Trays were sealed with Breathe Easy Sealing Tape (Diversified Biotech, Boston, MA). Results were recorded at 5 days.

Table 10. Pesticidal Activity on *T. ni*

Sample	# Dead/ Total	% Mortality
AXMI-014	13/13	100%
AXMI-008	6/6	100%
AXMI-009	17/17	100%
Negative Control	0/13	0%

Example 12. Expression of Delta-Endotoxin Genes in *Bacillus*

AXMI-004, AXMI-006, AXMI-007, AXMI-008, and AXMI-009 were amplified by PCR from the clones from Example 4, and cloned into the *Bacillus* Expression vector pAX916 by methods well known in the art. For AXMI-004 the resulting clone was designated pAX920. For AXMI-006 the resulting clone was designated pAX921. For AXMI-007 the resulting clone was designated pAX919. For AXMI-008 the resulting clone was designated pAX922. For AXMI-009 the resulting clone was designated pAX917. The resulting clones expressed the relevant protein when transformed into cells of a *cry(-) Bacillus thuringiensis* strain. The *Bacillus* strains containing delta-endotoxin genes and expressing the delta-endotoxin proteins may be cultured on a variety of conventional growth media. A *Bacillus* strain containing the desired gene was grown in CYS media (10 g/l Bacto-casitone; 3 g/l yeast extract; 6 g/l KH_2PO_4; 14 g/l K_2HPO_4; 0.5 mM $MgSO_4$; 0.05 mM $MnCl_2$; 0.05 mM $FeSO_4$), until sporulation was evident by microscopic examination. Samples were prepared, and delta-endotoxin proteins were tested for insecticidal activity in bioassays against important insect pests.

Methods

To prepare CYS media: 10 g/l Bacto-casitone; 3 g/l yeast extract; 6 g/l KH_2PO_4; 14 g/l K_2HPO_4; 0.5 mM $MgSO_4$; 0.05 mM $MnCl_2$; 0.05 mM $FeSO_4$. The CYS mix should be pH 7, if adjustment is necessary. NaOH or HCl are preferred. The media is then autoclaved and 100 ml of 10X filtered glucose is added after autoclaving. If the resultant solution is cloudy it can be stirred at room temperature to clear.

Example 13. N-terminal Amino Acid Sequence of AXMI-004 Expressed in *Bacillus*

Analysis of AXMI-004 expressed in *Bacillus* suggested that the protein product detected in these cultures may be reduced in size relative to the full-length AXMI-004 protein. Since many endotoxin proteins are cleaved at the N-terminus after expression in *Bacillus*, we determined the N-terminus of the AXMI-004 protein resulting from *Bacillus* expression. Protein samples from AXMI-004 were separated on PAGE gels, and the protein transferred to PVDF membrane by methods known in the art. The protein band corresponding to AXMI-004 was excised. The N-terminal amino acid sequence of this protein was determined by serial Edman degradation as known in the art. The sequence obtained was as follows:

ERFDKNDALE

Comparison of this amino acid sequence with the sequence of the full length AXMI-004 (SEQ ID NO:3) demonstrates that this amino sequence results from internal cleavage of the AXMI-004 after expression in *Bacillus*, resulting in a protein with an N-terminus corresponding to amino acid 28 of SEQ ID NO:3 (disclosed as SEQ ID NO:5).

Example 14. Bioassay of AXMI-004 on Insect Pests

Insecticidal activity of AXMI-004 was established utilizing accepted bioassay procedures using a sporulated *Bacillus* cell culture lysate expressing AXMI-004. The *Bacillus* culture was grown in 50 ml CYS media for both standard bioassay and LC_{50} bioassays. The cultures were then grown for 2 to 3 days at 30°C, 250 rpm until the cells were sporulated. Sporulation was determined by examining microscopically for the presence of spores. AXMI-004 protein samples were prepared by centrifugation of the sporulated cultures at 12,000 x g for 10 min. The pellet was collected and resuspended in 4 ml 20 mM Tris-HCl, pH 8.0. The suspension was sonicated for 20 seconds (at top power using a micro probe) while placing the tube on ice. The protein concentration of the sample was determined by electrophoresis on an SDS 4-20% gradient acrylamide gel along with a known quantity of bovine serum albumin (BSA) (Figure 8). The concentration of AXMI-004 was determined to be 0.4 µg/ul.

AXMI-004 insecticidal activity was tested using a surface treatment bioassay with artificial diet (Multiple Species diet, Southland Products, Lake Village, Arkansas) prepared as known in the art. Bioassays were carried out by applying the *Bacillus* culture expressing AXMI-004 to the diet surface and allowing the surface to air-dry. Standard bioassays utilized five eggs per well and LC_{50} bioassays utilized ten neonate insect larvae per well. The eggs or larvae were applied using a fine tip paintbrush. Standard surface bioassays were carried out in 24 well tissue culture plates. 40ul of each sample was applied to each well. Since each well has a surface area of 2 cm^2 (plate source), a 40 µl cell lysate sample contained approximately 0.4 ug/ul AXMI-004. Bioassays where the LC_{50} was determined were done in 48 well tissue culture plates, each well representing a surface area of 1 cm^2 (source) using approximately 20ul of 0.4 µg/ul AXMI-004 per well. The final amount of AXMI-004 protein in each bioassay was approximately 8 $\mu g/cm^2$. Bioassay trays were sealed with Breathe Easy Sealing Tape (Diversified Biotech, Boston MA). Control samples included media only samples, and wells that were not treated with samples. Bioassays were then held for five days in the dark at 25° C and 65% relative humidity and results recorded.

Table 11. Insecticidal Activity of AXMI-004

Insect (Latin Name)	Common Name	Activity of AXMI-004
Ostrinia nubilalis	European Corn Borer	100% mortality
Agrotis ipsilon	Black Cutworm	Stunted
Heliothis zea	Corn Earworm	Stunted
Spodoptera frugiperda	Fall Armyworm	Stunted
Heliothis virescens	Tobacco Budworm	100% mortality
Pectinophora gossypiella	Pink Bollworm	75% mortality
Manduca sexta	Tobacco Hornworm	100% mortality
Trichoplusia ni	Cabbage Looper	100% mortality

AXMI-004 showed strong insecticidal activity (100% mortality) against *Ostrinia nubilalis* and *Heliothis virescens*. AXMI-004 also showed insecticidal activity of 50-75% mortality against *Pectinophora gossypiella*. A concentration of 43 μg/cm^2 AXMI-004 gave 70% mortality against *Pectinophora gossypiella*. AXMI-004 severely stunted the growth of *Agrotis ipsilon*, *Heliothis zea*, and *Spodoptera frugiperda*.

Example 15. Quantitation of AXMI-004 Insecticidal Activity against *Heliothis virescens* and *Ostrinia nubilalis*

The LC_{50} of AXMI-004 protein on *Ostrinia nubilalis* and *Heliothis virescens* larvae were determined by testing a range of AXMI-004 protein concentrations in insect bioassays, and applying these protein samples to the surface of insect diet. Mortality was recorded at each protein concentration and analyzed using a Probit analysis program. Results were significant at the 95% confidence interval. Since assays were performed by surface contamination, LC_{50}s were determined assuming that the entire protein sample remained at the surface during the assay, with little diffusion below the level ingested by the insects. Thus, the values determined may somewhat underestimate the toxicity of the AXMI-004 protein on the tested insects.

Table 12. LC_{50} of AXMI-004 on *Ostrinia nubilalis*

AXMI-004 (μg/ml)	# dead/total	% Mortality
1000	40/46	86.9
500	28/45	62.2
250	16/43	32.7
125	12/38	31.6

LC_{50}= 297 ng/cm^2 ; 95% CI = 218-384.

Table 13. $LC5_0$ of AXMI-004 on *Heliothis virescens*

AXMI-004 (µg/ml)	# dead/total	% Mortality
8000	35/47	74.5
4000	26/44	59.1
2000	18/42	42.9
1000	6/27	22.2
500	4/36	11.1
250	2/37	5.4

LC_{50}= 2874 ng/cm^2; 95% CI = 2189-3933

Example 16. Quantitation of AXMI-004, AXMI-006, AXMI-007, and AXMI-009 Insecticidal Activity against *Lygus lineolaris*

Bacterial lysates were prepared by growing the *Bacillus* in 50 ml of CYS media for 60 hours. The *Bacillus* culture was then centrifuged at 12,000 rpm for ten minutes and the supernatant discarded. The pellet was resuspended in 5 ml of 20 mM Tris HCl at pH 8.

Bioassays were performed by cutting both the tip and the cap off an Eppendorf tube to form a feeding chamber. The insecticidal protein or control was presented to the insect in a solution that was poured into the cap and covered with parafilm (Pechiney Plastic Packaging, Chicago IL) that the insect could pierce upon feeding. The Eppendorf tube was placed back on the cap top down and 1st or 2nd instar *Lygus* nymphs were placed into the Eppendorf chamber with a fine tip brush. The cut Eppendorf tube tip was sealed with parafilm creating an assay chamber. The resultant assay chamber was incubated at ambient temperature cap side down. Insecticidal proteins were tested in a solution of 15% glucose at a concentration of 6.6 ug/ml.

Table 14. Insecticidal Activity on *Lygus lineolaris*

Protein	No. Dead/Total	% Mortality
AXMI-004	2/4	50%
AXMI-006	1/6	16.7%
AXMI-007	3/6	50%
AXMI-009	2/4	50%
Control	0/9	0%

Example 17. Bioassay of AXMI-008 on *Tenebrio molitor*

Samples of *Bacillus* cultures expressing AXMI-008 were prepared and tested for pesticidal activity on *Tenebrio molitor*. When pAX 922 is prepared as an insoluble fraction at pH 4.0 it showed activity against commonly called the yellow mealworm.

Samples of AXMI-008 were prepared from a culture of a *Bacillus* strain containing pAX 922. The bioassay sample was prepared by growing a culture in CYS media for 4 days, until sporulation. The sample was centrifuged at 10,000 rpm for 10 minutes and the supernatant discarded. The pellet was washed in 20mM Tris pH 8 and spun at 10,000 rpm for 10 minutes. The supernatant was discarded and the pellet resuspended in 3 mls of 50 mM Sodium Citrate and 25 mM Sodium Chloride with 2mM DTT at pH 4. The sample was incubated at 37° C for 1 hour. After incubation the sample was spun at 13,000 rpm for 10 minutes and the supernatant discarded. The pellet was resuspended in 50 mM Sodium Citrate and 25 mM Sodium Chloride at pH 4.

Bioassays of samples on *Tenebrio molitor* were performed on an artificial diet (Southern Corn Rootworm Diet, Bioserv, Frenchtown, NJ, #F9757B) in 24 well tissue culture plates. The sample was applied as a surface treatment with a concentration of Axmi008 at 8 ug/cm^2 and allowed to air dry. The insects were applied using a fine tip brush. Bioassay trays were sealed with Breathe Easy Sealing Tape (Diversified Biotech, Boston, MA) and incubated without light at 65% relative humidity, 25° C. for seven days and results recorded.

Table 15. Pesticidal Activity of AXMI-008 on *T. molitor*

Sample	# Dead/ Total	% Mortality
AXMI-008	3 of 4	75%*

* Remaining *Tenebrio molitor* was stunted. Stunting is observed as reduced larval size and growth, and severely reduced or minimal feeding. The insect may also demonstrate avoidance of the treated diet compared to the untreated diet.

Example 18. Bioassay of AXMI-009 Protein on Coleopteran Pests

Bioassays of AXMI-009 protein preparations were performed by pipetting 40 µl of insoluble fraction onto a 2 cm^2 diet surface for a final total protein concentration of 8µg/cm^2. *Diabrotica virgifera virgifera* and *Diabrotica undecimpunctata* were tested using Southern Corn Rootworm Diet (Bioserv, Frenchtown, NJ, #F9757B). Bioassays were carried out by applying the *Bacillus* culture expressing AXMI-009 to the diet surface and allowing the diet surface to dry. Bioassays were performed in 24 well tissue culture plates. Standard bioassays utilized 25 eggs per well. The eggs were applied in a solution containing 0.1% agar and 30 ug/ml nystatin. Trays were sealed with Breathe Easy Sealing Tape (Diversified Biotech, Boston, MA) and the lids placed back on the trays. Bioassays were incubated without light at 65% Relative Humidity (RH), 25° C for seven days. Activity was seen with the insoluble fraction for both *Diabrotica virgifera virgifera* and *Diabrotica undecimpunctata.* Controls were a media only, buffer of 1 mM Tris at pH 10.5, and the *Bacillus* expression vector pAX916.

Table 16. Western Corn Rootworm (*Diabrotica virgifera virgifera*)

	# Dead/Total	% Mortality
AXMI-009 insoluble fraction	38/38	100%
Media only (CYS)	1/25	4%
Buffer	2/24	8.3%
Vector (pAX916)	1/12	8.3%

Table 17. Southern Corn Rootworm (*Diabrotica undecimpunctata*)

	# Dead/Total	% Mortality
AXMI-009 insoluble fraction	20/20	100%
Media only (CYS)	0/20	0%
Buffer	0/23	0%
Vector (pAX916)	0/19	0%

Example 19. Vectoring for Plant Expression

The delta-endotoxin coding region DNA is operably connected with appropriate promoter and terminator sequences for expression in plants. Such sequences are well known in the art and may include the rice actin promoter or maize ubiquitin promoter for expression in monocots, the *Arabidopsis* UBQ3 promoter or CaMV 35S promoter for expression in dicots, and the nos or PinII terminators. Techniques for producing and confirming promoter – gene – terminator constructs also are well known in the art.

The plant expression cassettes described above are combined with an appropriate plant selectable marker to aid in the selections of transformed cells and tissues, and ligated into plant transformation vectors. These may include binary vectors from *Agrobacterium*-mediated transformation or simple plasmid vectors for aerosol or biolistic transformation.

Example 20. Transformation of Maize Cells

Maize ears are collected 8-12 days after pollination. Embryos are isolated from the ears, and those embryos 0.8-1.5 mm in size are used for transformation. Embryos are plated scutellum side-up on a suitable incubation media, such as DN62A5S media (3.98 g/L N6 Salts; 1 mL/L (of 1000x Stock) N6 Vitamins; 800 mg/L L-Asparagine; 100 mg/L Myo-inositol; 1.4 g/L L-Proline; 100 mg/L Casaminoacids; 50 g/L sucrose; 1 mL/L (of 1 mg/mL Stock) 2,4-D), and incubated overnight at 25°C in the dark.

The resulting explants are transferred to mesh squares (30-40 per plate), transferred onto osmotic media for 30-45 minutes, then transferred to a beaming plate (see, for example, PCT Publication No. WO/0138514 and U.S. Patent No. 5,240,842).

DNA constructs designed to express the delta-endotoxin in plant cells are accelerated into plant tissue using an aerosol beam accelerator, using conditions

essentially as described in PCT Publication No. WO/0138514. After beaming, embryos are incubated for 30 min on osmotic media, then placed onto incubation media overnight at 25°C in the dark. To avoid unduly damaging beamed explants, they are incubated for at least 24 hours prior to transfer to recovery media. Embryos are then spread onto recovery period media, for 5 days, 25°C in the dark, then transferred to a selection media. Explants are incubated in selection media for up to eight weeks, depending on the nature and characteristics of the particular selection utilized. After the selection period, the resulting callus is transferred to embryo maturation media, until the formation of mature somatic embryos is observed. The resulting mature somatic embryos are then placed under low light, and the process of regeneration is initiated by methods known in the art. The resulting shoots are allowed to root on rooting media, and the resulting plants are transferred to nursery pots and propagated as transgenic plants.

Materials

DN62A5S Media

Components	per liter	Source
Chu'S N6 Basal Salt Mixture (Prod. No. C 416)	3.98 g/L	Phytotechnology Labs
Chu's N6 Vitamin Solution (Prod. No. C 149)	1 mL/L (of 1000x Stock)	Phytotechnology Labs
L-Asparagine	800 mg/L	Phytotechnology Labs
Myo-inositol	100 mg/L	Sigma
L-Proline	1.4 g/L	Phytotechnology Labs
Casaminoacids	100 mg/L	Fisher Scientific
Sucrose	50 g/L	Phytotechnology Labs
2,4-D (Prod. No. D-7299)	1 mL/L (of 1 mg/mL Stock)	Sigma

Adjust the pH of the solution to pH to 5.8 with 1N KOH/1N KCl, add Gelrite (Sigma) to 3g/L, and autoclave. After cooling to 50°C, add 2 ml/L of a 5 mg/ml stock solution of Silver Nitrate (Phytotechnology Labs). Recipe yields about 20 plates.

Example 21. Transformation into Plant Cells by *Agrobacterium*-Mediated Transformation

Ears are collected 8-12 days after pollination. Embryos are isolated from the ears, and those embryos 0.8-1.5 mm in size are used for transformation. Embryos are plated scutellum side-up on a suitable incubation media, and incubated overnight at 25°C in the dark. However, it is not necessary *per se* to incubate the embryos overnight. Embryos are contacted with an *Agrobacterium* strain containing the appropriate vectors for Ti plasmid mediated transfer for 5-10 min, and then plated onto co-cultivation media for 3 days (25°C in the dark). After co-cultivation, explants are transferred to recovery period media for five days (at 25°C in the dark). Explants are incubated in selection media for up to eight weeks, depending on the nature and characteristics of the particular selection utilized. After the selection period, the resulting callus is transferred to embryo maturation media, until the formation of mature somatic embryos is observed. The resulting mature somatic embryos are then placed under low light, and the process of regeneration is initiated as known in the art. The resulting shoots are allowed to root on rooting media, and the resulting plants are transferred to nursery pots and propagated as transgenic plants.

Conclusions

The delta-endotoxin proteins of the present invention have activity against numerous pests, as shown in the examples above. AXMI-004 has pesticidal activity against pests including *Ostrinia nubilalis, Agrotis ipsilon, Heliothis zea, Spodoptera frugiperda, Heliothis virescens, Pectinophora gossypiella, Manduca Sexta, Trichoplasia ni*, and *Lygus lineolaris*. AXMI-006 has pesticidal activity against pests including *Heliothis virescens, Spodoptera frugiperda*, and *Lygus lineolaris*. AXMI-007 has pesticidal activity against pests including *Lygus lineolaris*. AXMI-008 has pesticidal activity against pests including *Tenebrio molitor* and *Trichoplusia ni*. AXMI-009 has pesticidal activity against pests including *Lygus lineolaris, Trichoplusia ni, Diabrotica virgifera virgifera,* and *Diabrotica undecimpunctata*. AXMI-014 has pesticidal activity against pests including *Trichoplusia ni*.

All publications and patent applications mentioned in the specification are indicative of the level of skill of those skilled in the art to which this invention

pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious that certain changes and modifications may be practiced within the scope of the appended claims.

THAT WHICH IS CLAIMED:

1. An isolated nucleic acid molecule selected from the group consisting of:

a) a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1, 2, 4, 6, 8, 10, 12, 13, 15, 17, 19, 21, 23, 25, 26, or 28;

b) a nucleic acid molecule comprising a nucleotide sequence having at least 95% sequence identity to the nucleotide sequence of SEQ ID NO:1, 2, 4, 6, 8, 10, 12, 13, 15, 17, 19, 21, 23, 25, 26, or 28, wherein said nucleotide sequence encodes a polypeptide having pesticidal activity;

c) a nucleic acid molecule which encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 27, or 29;

d) a nucleic acid molecule comprising a nucleotide sequence encoding a polypeptide having at least 95% amino acid sequence identity to the amino acid sequence of SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 27, or 29, wherein said polypeptide has pesticidal activity; and,

e) a complement of any of a)-d).

2. An isolated nucleic acid molecule of claim 1, wherein said nucleotide sequence is a synthetic sequence that has been designed for expression in a plant.

3. The nucleic acid molecule of claim 2, wherein said synthetic sequence has an increased GC content.

4. A vector comprising the nucleic acid molecule of claim 1.

5. The vector of claim 4, further comprising a nucleic acid molecule encoding a heterologous polypeptide.

6. A host cell that contains the vector of claim 4.

7. The host cell of claim 6 that is a bacterial host cell.

8. The host cell of claim 6 that is a plant cell.

9. A transgenic plant comprising the host cell of claim 8.

10. The transgenic plant of claim 9, wherein said plant is selected from the group consisting of maize, sorghum, wheat, sunflower, tomato, crucifers, peppers, potato, cotton, rice, soybean, sugarbeet, sugarcane, tobacco, barley, and oilseed rape.

11. Transgenic seed of a plant of claim 9.

12. An isolated polypeptide selected from the group consisting of:

a) a polypeptide comprising the amino acid sequence of SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 27, or 29;

b) a polypeptide encoded by the nucleotide sequence of SEQ ID NO:1, 2, 4, 6, 8, 10, 12, 13, 15, 17, 19, 21, 23, 25, 26, or 28, wherein said polypeptide has pesticidal activity;

c) a polypeptide comprising an amino acid sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 27, or 29, wherein said polypeptide has pesticidal activity; and,

d) a polypeptide that is encoded by a nucleotide sequence that is at least 95% identical to the nucleotide sequence of SEQ ID NO:1, 2, 4, 6, 8, 10, 12, 13, 15, 17, 19, 21, 23, 25, 26, or 28.

13. The polypeptide of claim 12, further comprising a heterologous amino acid sequence.

14. An antibody that selectively binds to a polypeptide of claim 12.

15. A composition comprising the polypeptide of claim 12.

16. The composition of claim 15, wherein said composition is selected from the group consisting of a powder, dust, pellet, granule, spray, emulsion, colloid, and solution.

17. The composition of claim 15, wherein said composition is prepared by desiccation, lyophilization, homogenization, extraction, filtration, centrifugation, sedimentation, or concentration of a culture of *Bacillus thuringiensis* cells.

18. The composition of claim 15, comprising from about 1% to about 99% by weight of said polypeptide.

19. A method for producing a polypeptide with pesticidal activity, comprising culturing the host cell of claim 6 under conditions in which a nucleic acid molecule encoding the polypeptide is expressed, said polypeptide being selected from the group consisting of:

a) a polypeptide comprising the amino acid of SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 27, or 29;

b) a polypeptide encoded by the nucleotide sequence of SEQ ID NO:1, 2, 4, 6, 8, 10, 12, 13, 15, 17, 19, 21, 23, 25, 26, or 28, wherein said polypeptide has pesticidal activity;

c) a polypeptide comprising an amino acid sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 27, or 29, wherein said polypeptide has pesticidal activity; and,

d) a polypeptide that is encoded by a nucleotide sequence that is at least 95% identical to a nucleotide sequence of SEQ ID NO:1, 2, 4, 6, 8, 10, 12, 13, 15, 17, 19, 21, 23, 25, 26, or 28.

20. A method for controlling a lepidopteran or coleopteran pest population comprising contacting said population with a pesticidally-effective amount of a polypeptide of claim 12.

21. A method for killing a lepidopteran or coleopteran pest, comprising contacting said pest with, or feeding to said pest, a pesticidally-effective amount of a polypeptide of claim 12.

22. A plant having stably incorporated into its genome a DNA construct comprising a nucleotide sequence that encodes a protein having pesticidal activity, wherein said nucleotide sequence is selected from the group consisting of:

a) a nucleotide sequence of SEQ ID NO:1, 2, 4, 6, 8, 10, 12, 13, 15, 19, 21, 23, 25, 26, or 28;

b) a nucleotide sequence having at least 95% sequence identity to a nucleotide sequence of SEQ ID NO:1, 2, 4, 6, 8, 10, 12, 13, 15, 19, 21, 23, 25, 26, or 28, wherein said nucleotide sequence encodes a polypeptide having pesticidal activity;

c) a nucleotide sequence encoding a polypeptide comprising an amino acid sequence of SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 20, 22, 24, 27, or 29; and,

d) a nucleotide sequence encoding a polypeptide having at least 95% amino acid sequence identity to the amino acid sequence of SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 20, 22, 24, 27, or 29, wherein said polypeptide has pesticidal activity;

wherein said nucleotide sequence is operably linked to a promoter that drives expression of a coding sequence in a plant cell.

23. The plant of claim 22, wherein said plant further comprises the nucleotide sequence of SEQ ID NO:17.

24. A plant cell having stably incorporated into its genome a DNA construct comprising a nucleotide sequence that encodes a protein having pesticidal activity, wherein said nucleotide sequence is selected from the group consisting of:

a) a nucleotide sequence of SEQ ID NO:1, 2, 4, 6, 8, 10, 12, 13, 15, 19, 21, 23, 25, 26, or 28;

b) a nucleotide sequence having at least 95% sequence identity to a nucleotide sequence of SEQ ID NO:1, 2, 4, 6, 8, 10, 12, 13, 15, 19, 21, 23, 25, 26, or 28, wherein said nucleotide sequence encodes a polypeptide having pesticidal activity;

c) a nucleotide sequence encoding a polypeptide comprising an amino acid sequence of SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 20, 22, 24, 27, or 29; and,

d) a nucleotide sequence encoding a polypeptide having at least 95% amino acid sequence identity to the amino acid sequence of SEQ ID NO:3, 5, 7, 9, 11, 14, 16, 20, 22, 24, 27, or 29, wherein said polypeptide has pesticidal activity;

wherein said nucleotide sequence is operably linked to a promoter that drives expression of a coding sequence in a plant cell.

25. The plant cell of claim 24, wherein said plant cell further comprises the nucleotide sequence of SEQ ID NO:17.

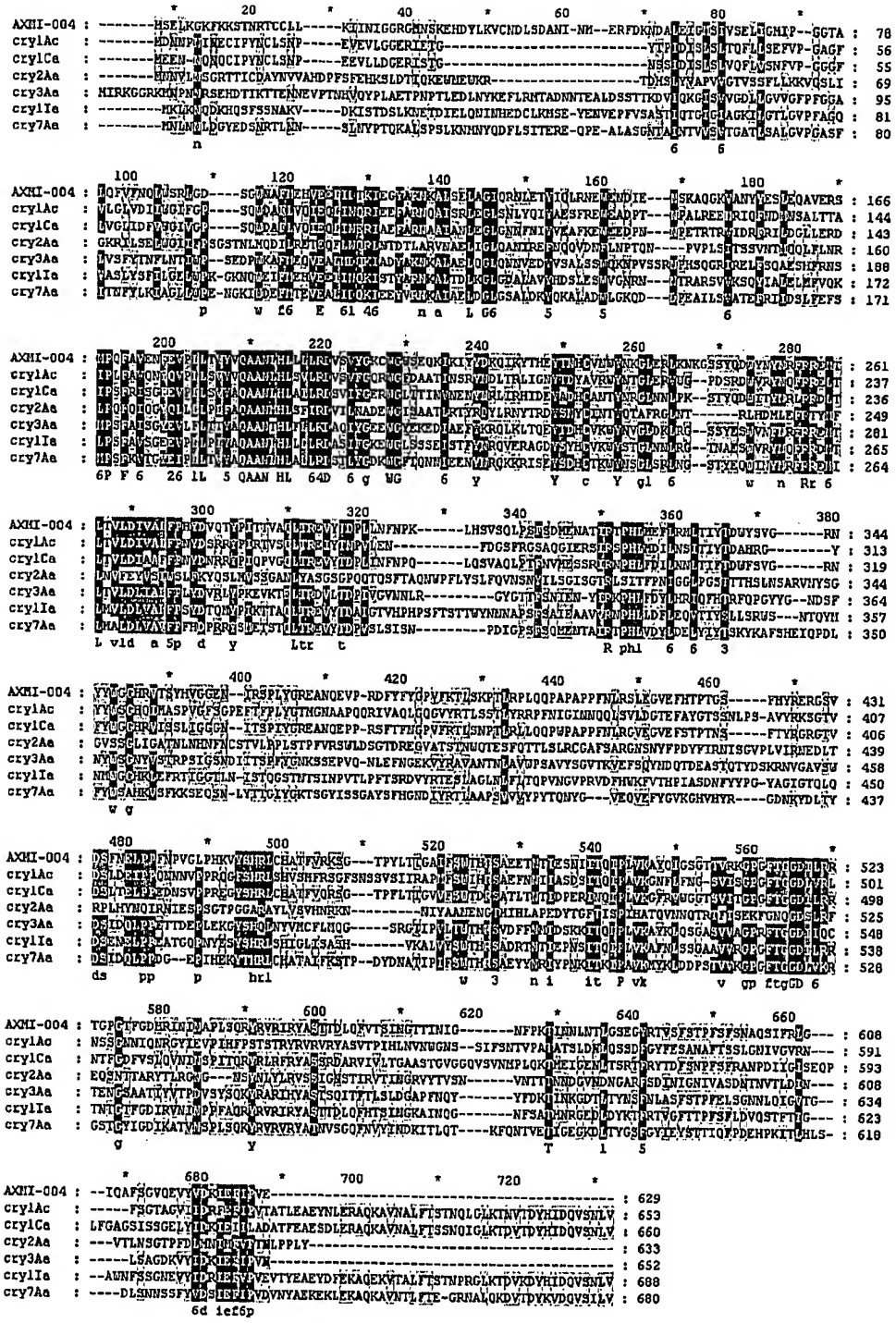

Fig. 1

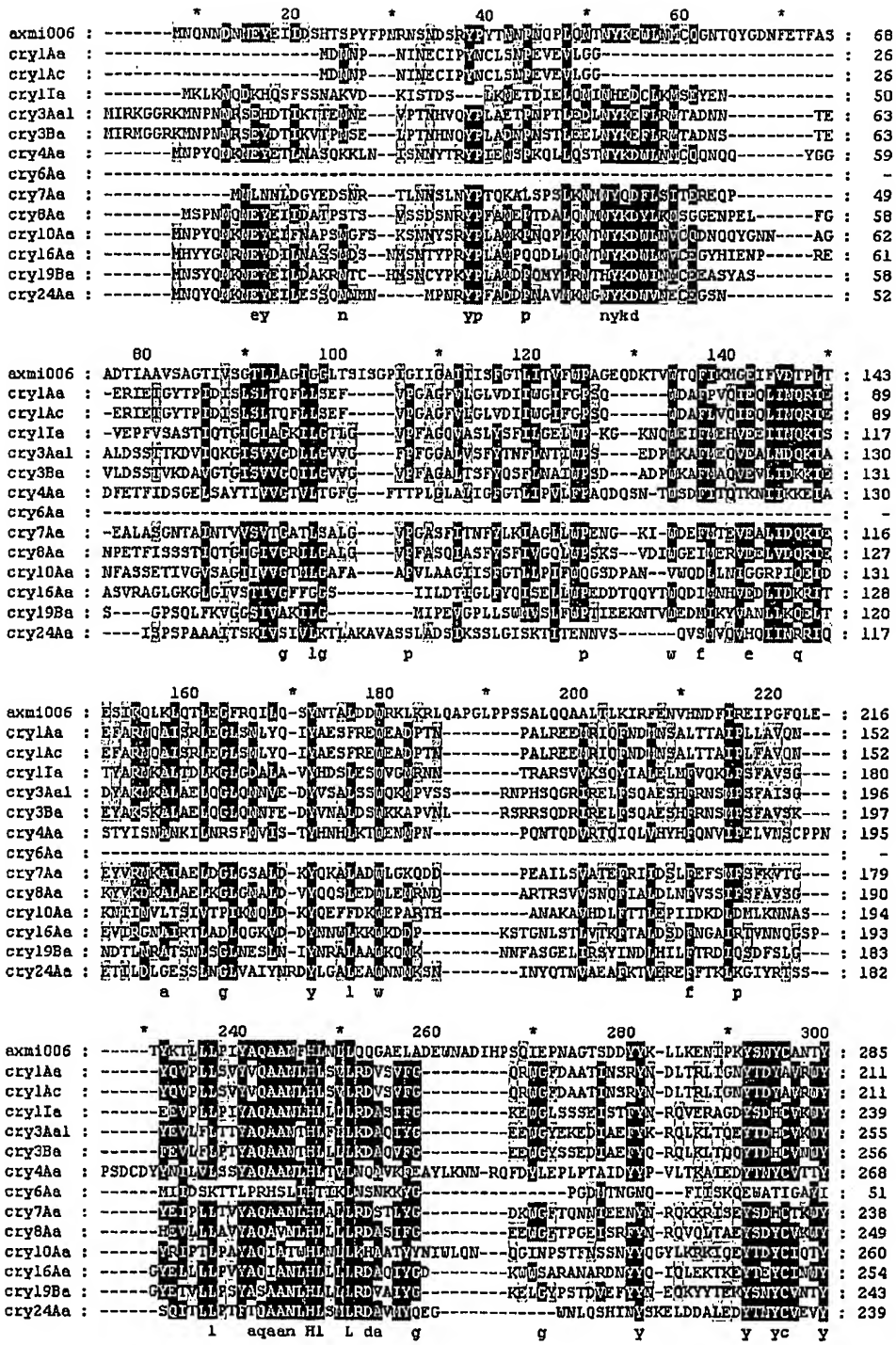

Fig.2A

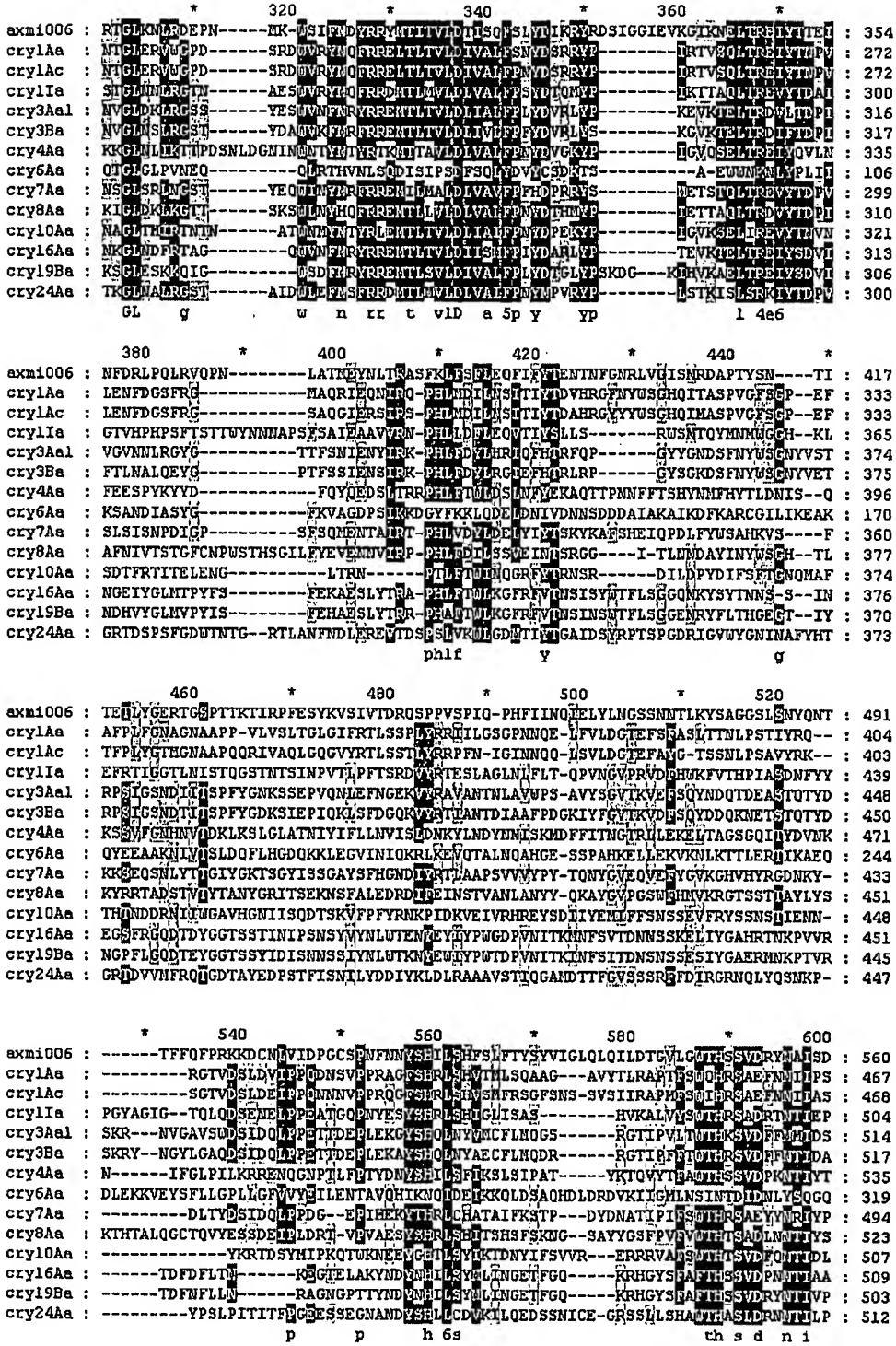

Fig.2B

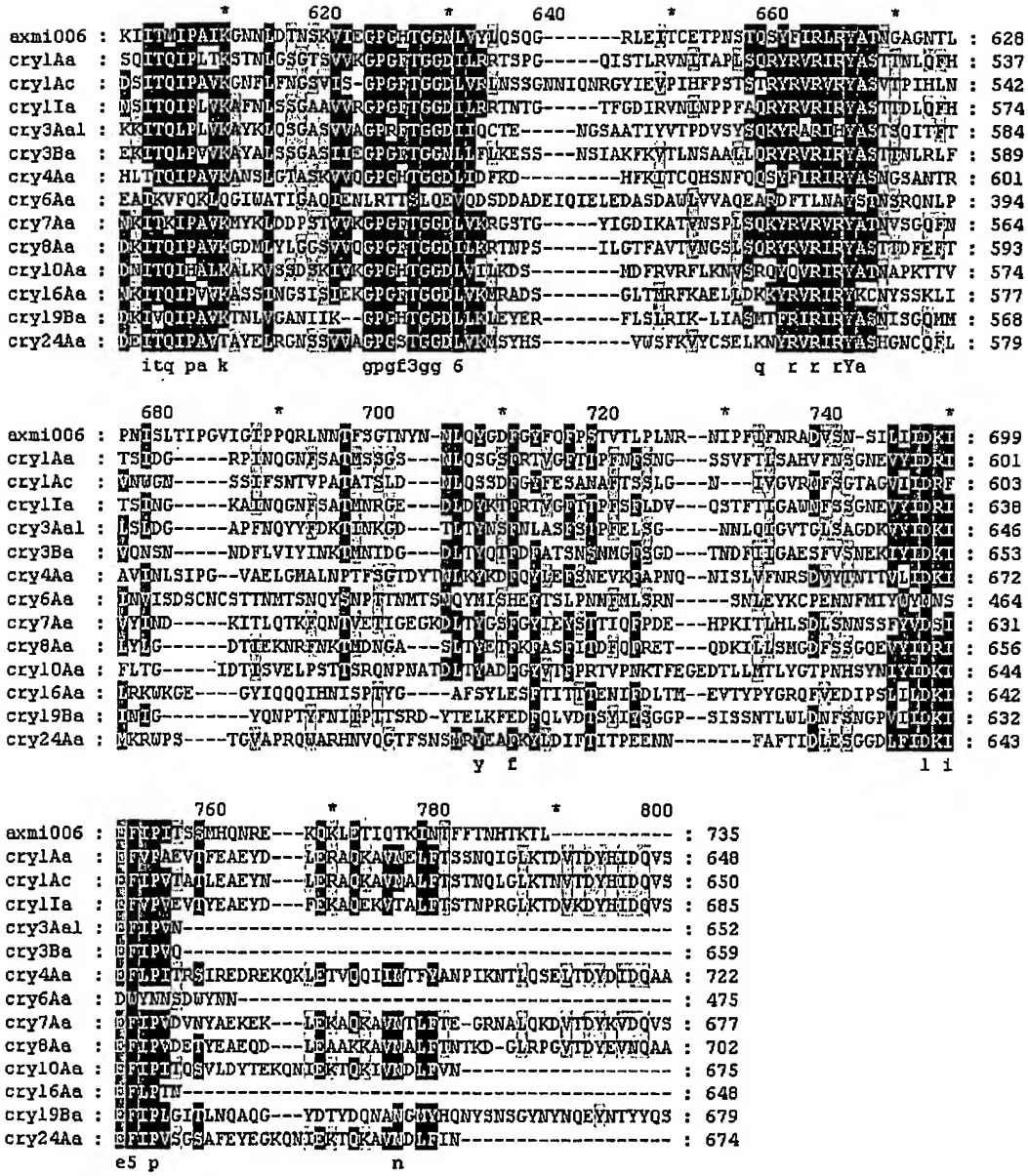

Fig.2C

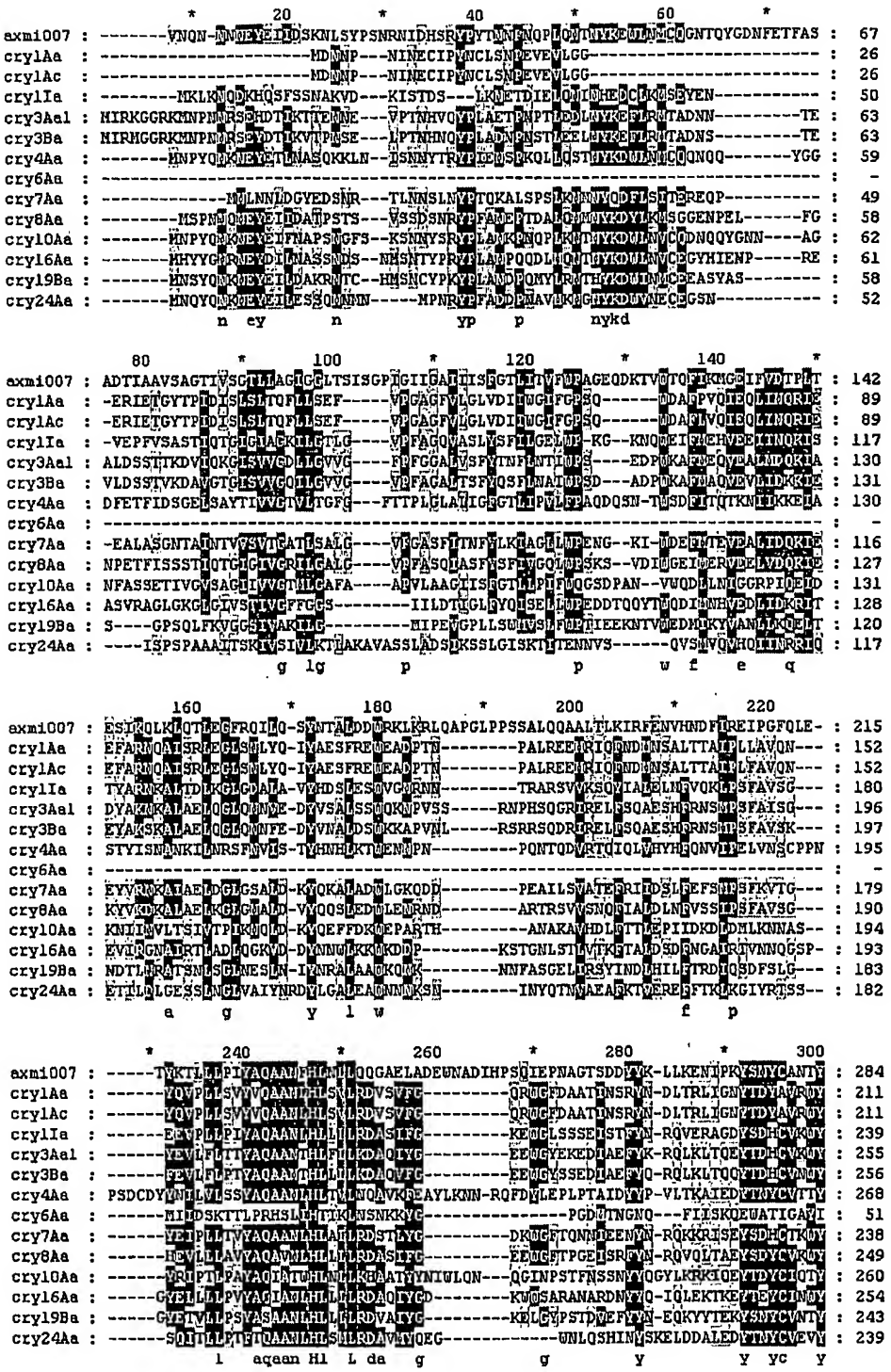

Fig. 3A

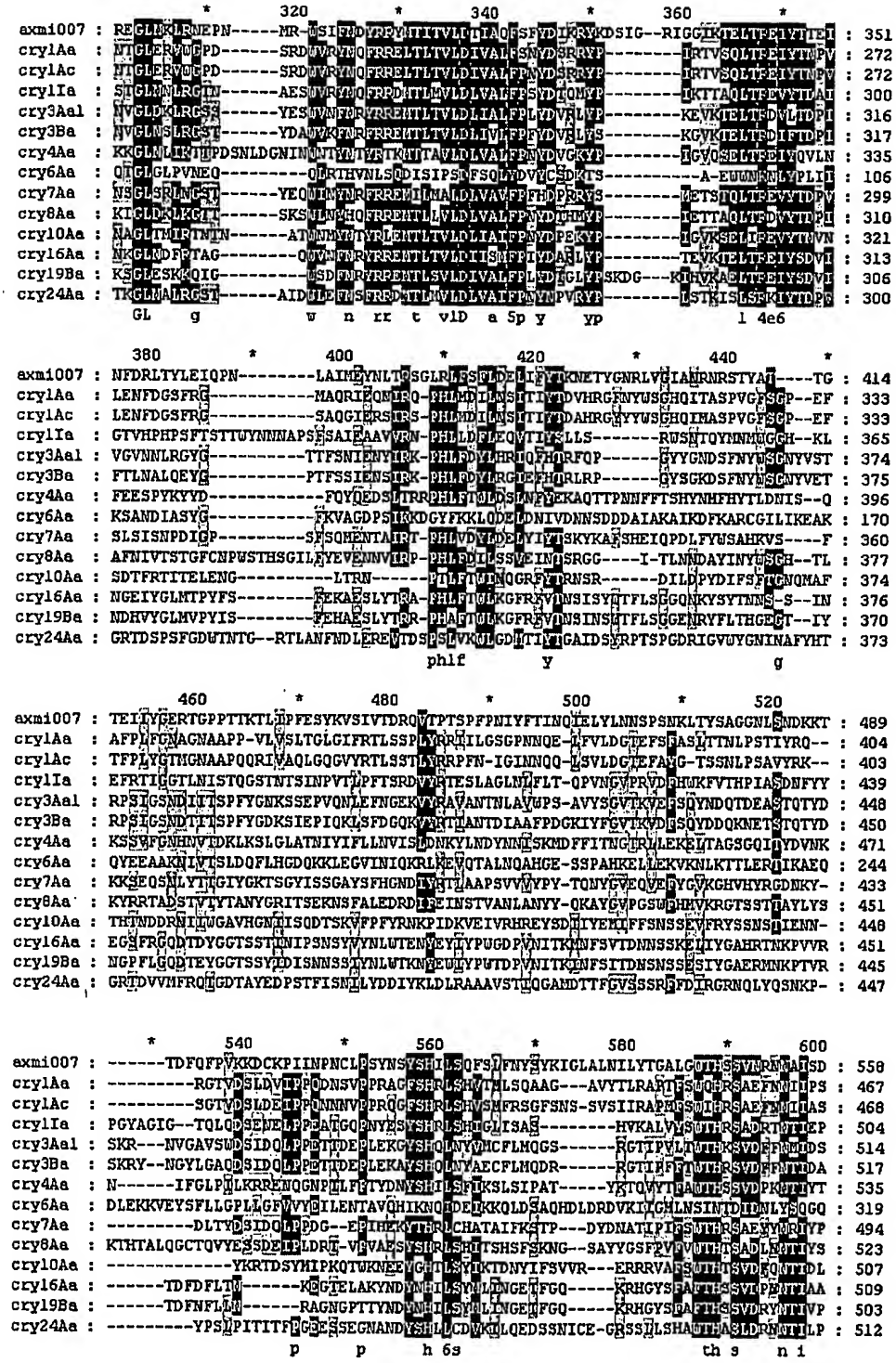

Fig. 3B

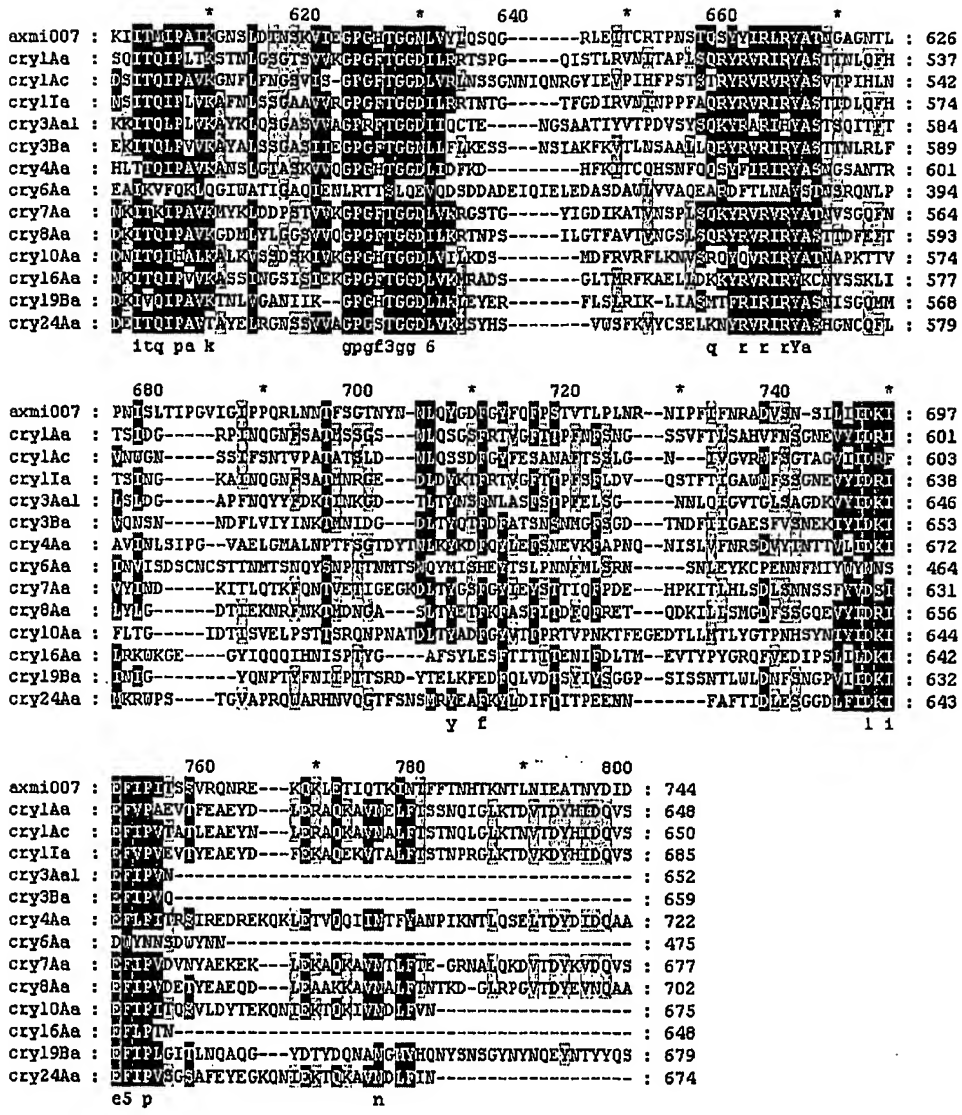

Fig. 3C

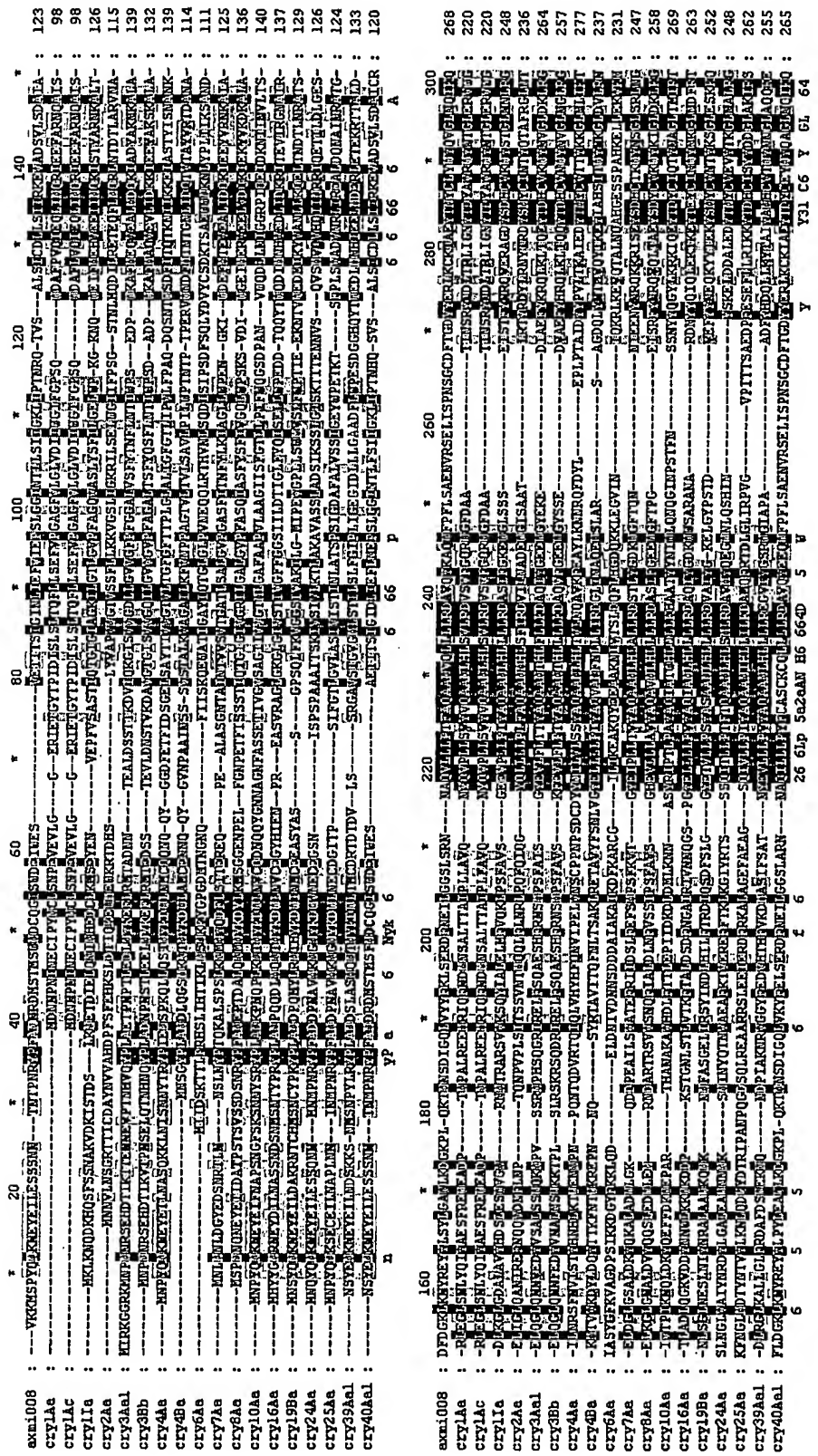

Fig. 4A

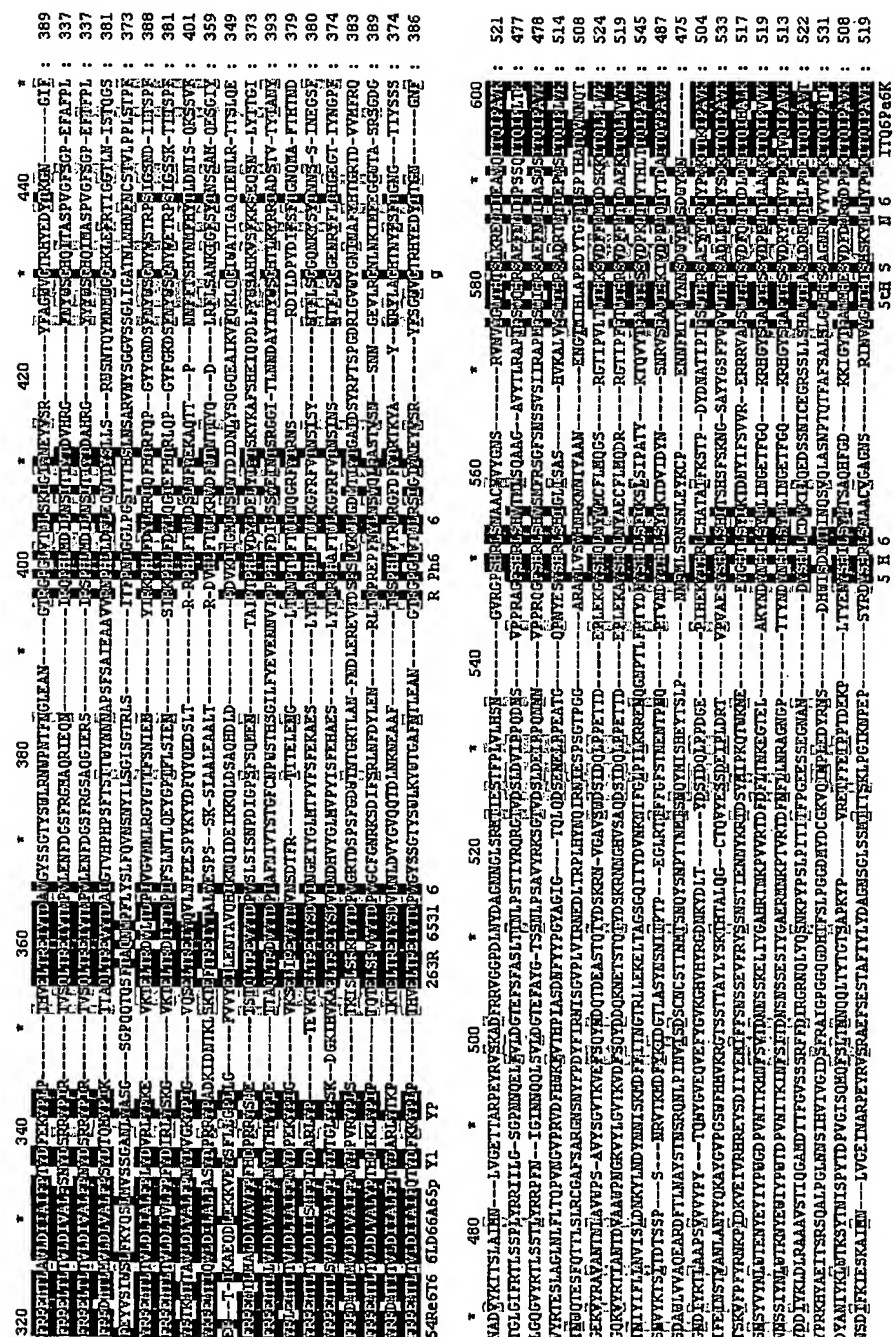

Fig. 4B

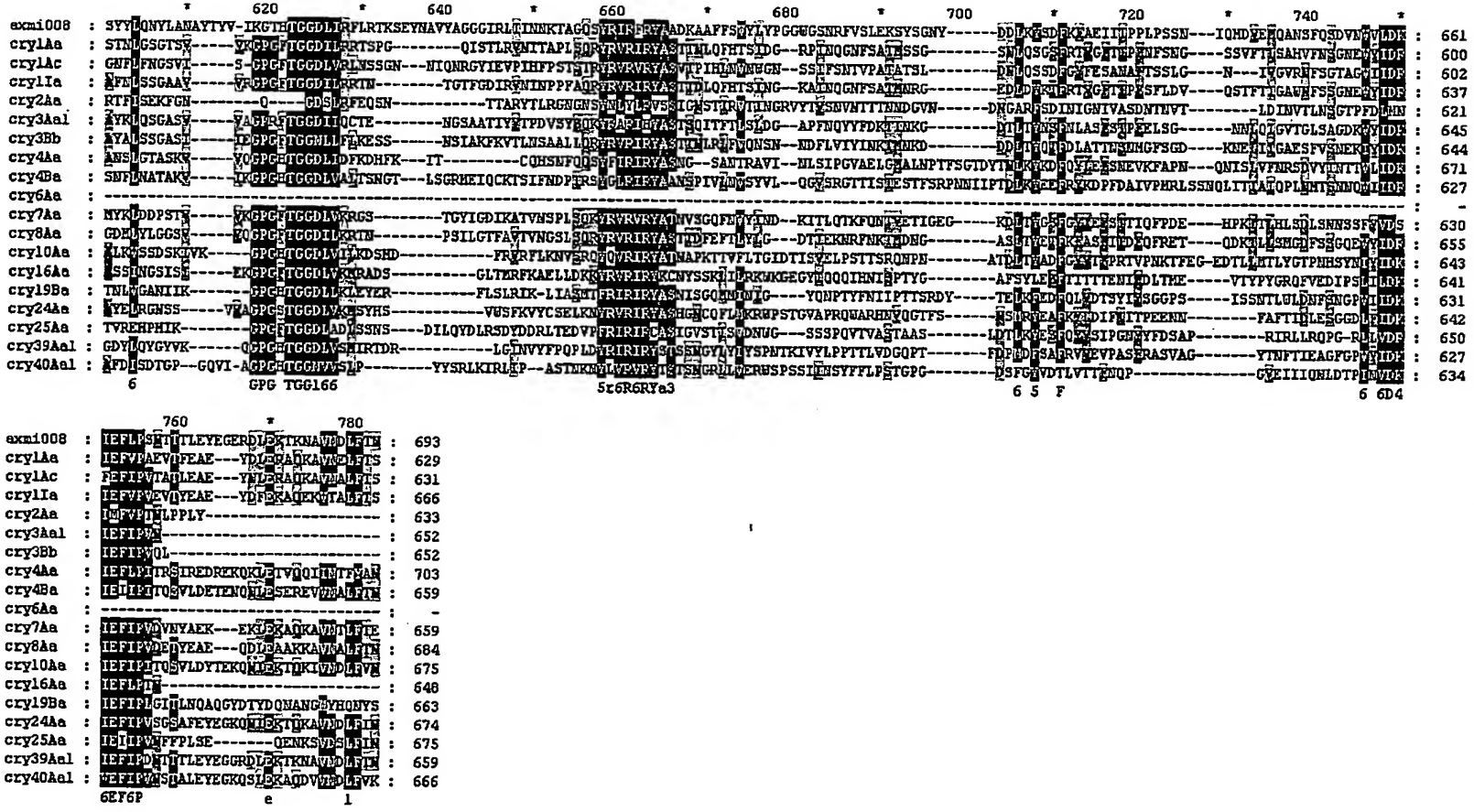

Fig. 4C

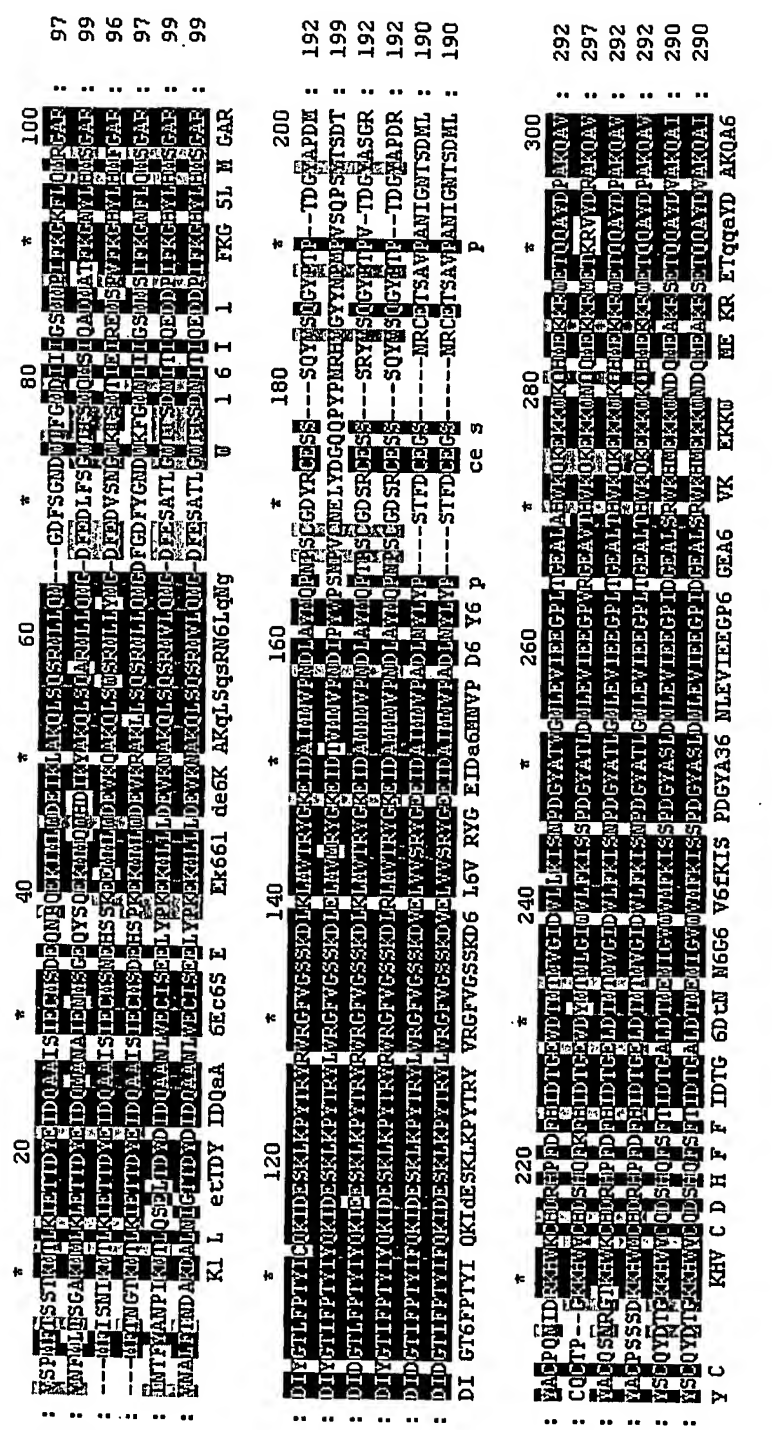

Fig. 5A

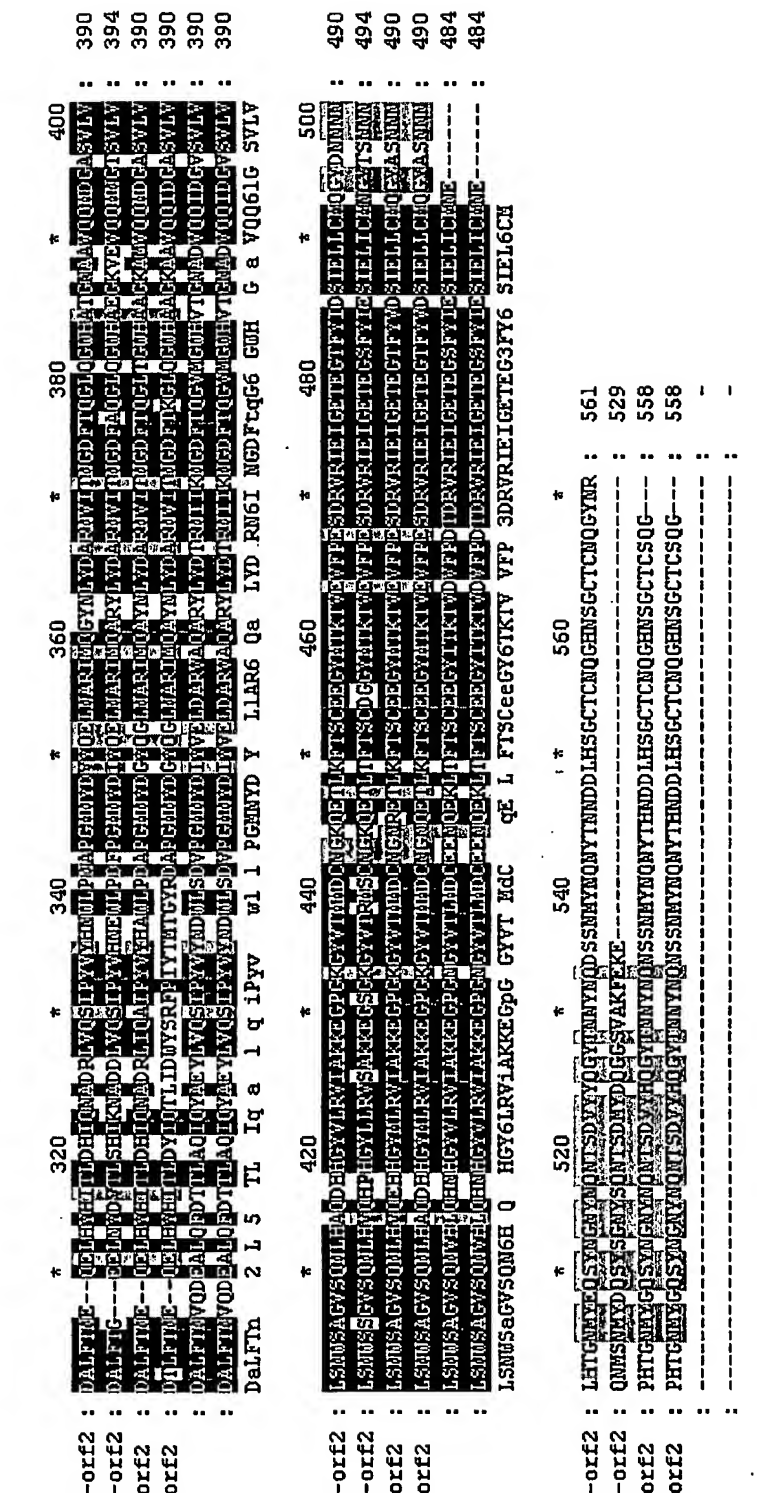

Fig. 5B

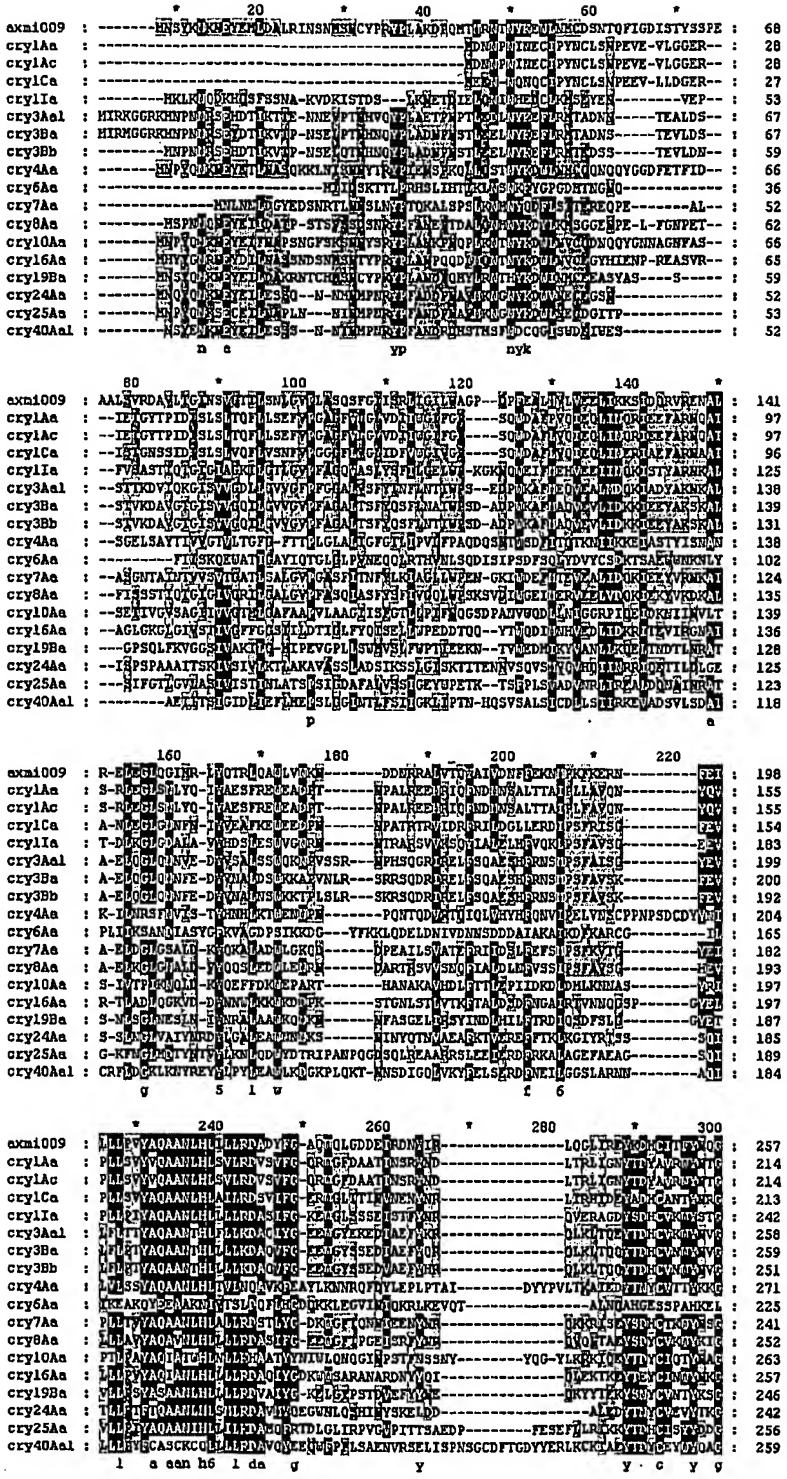

Fig. 6A

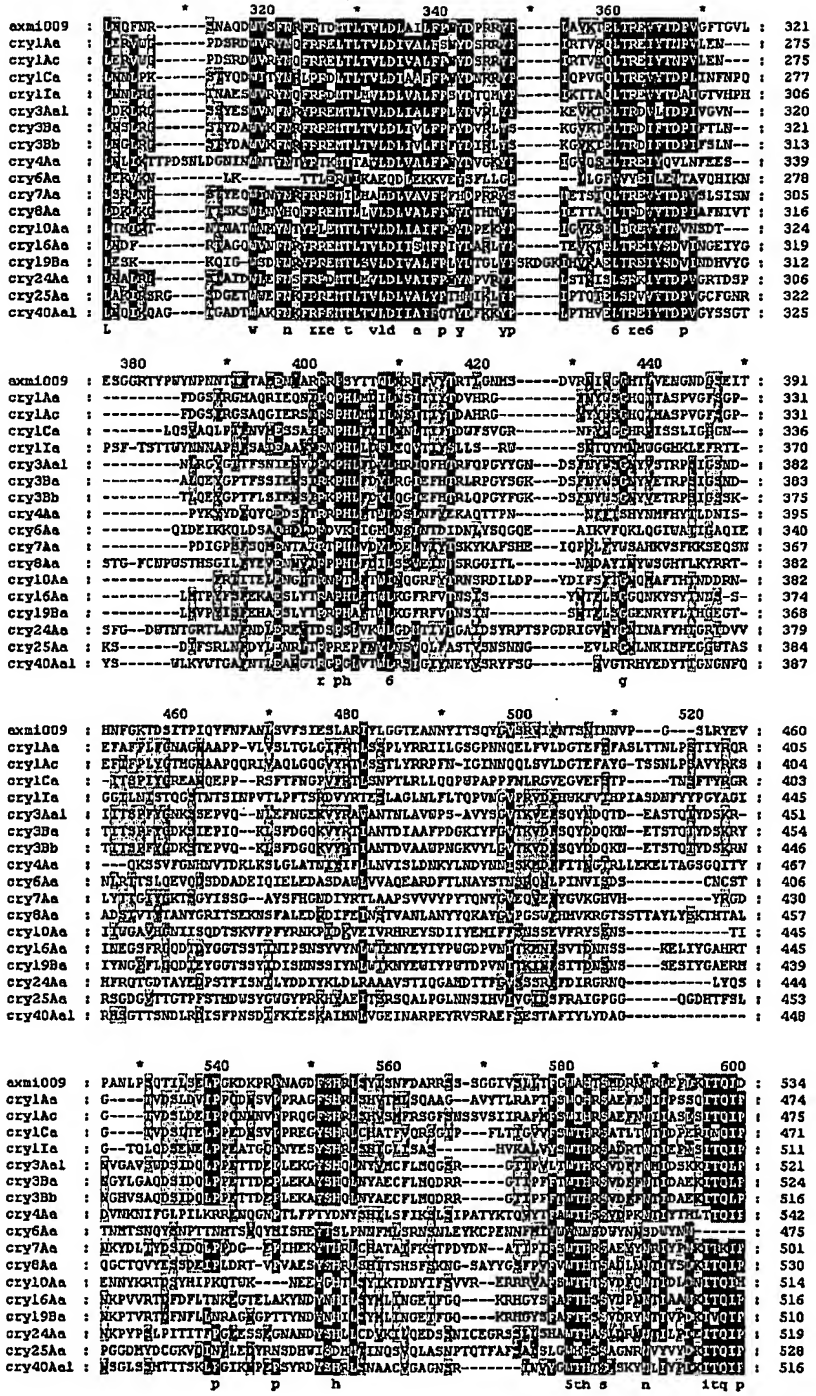

Fig. 6B

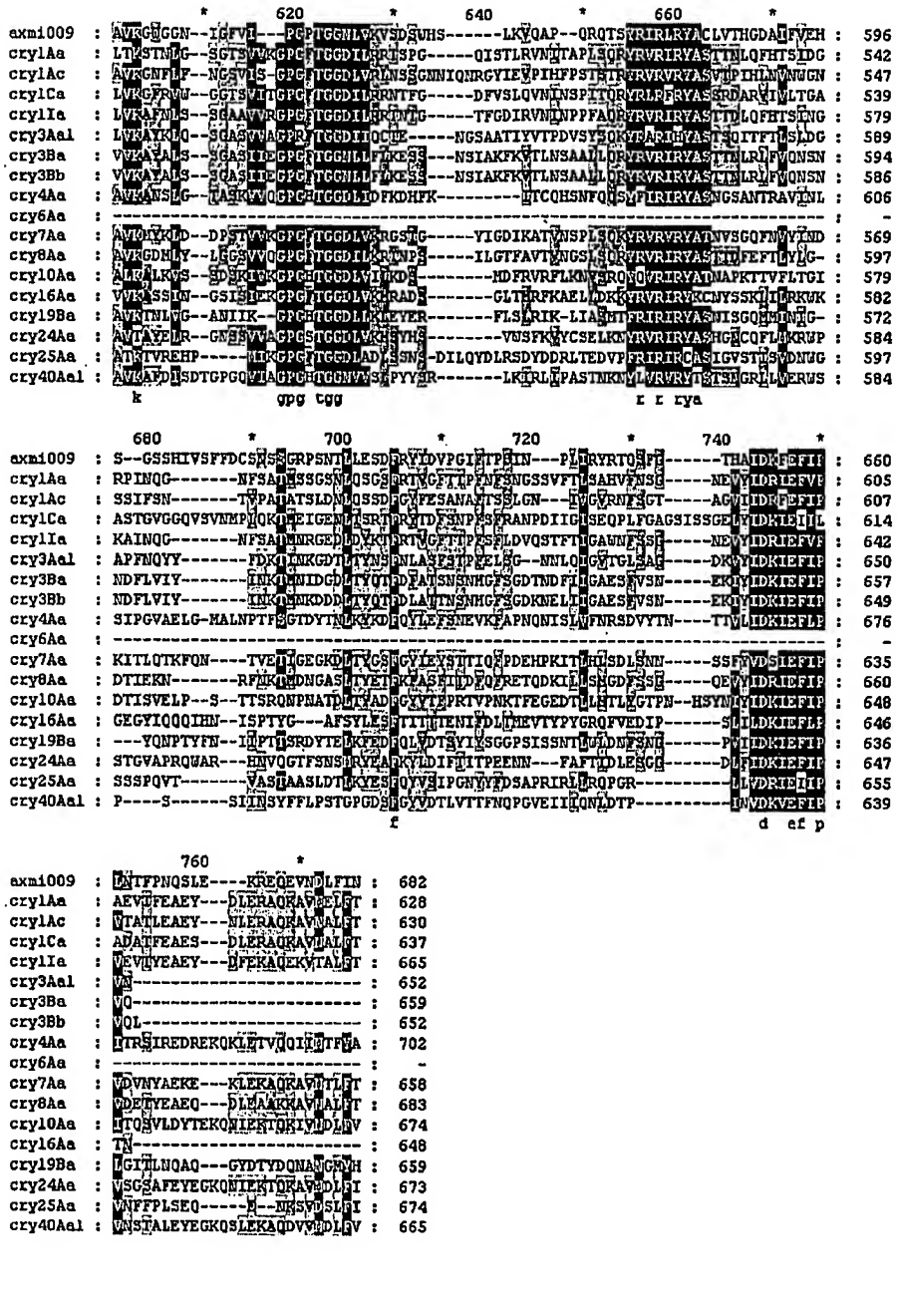

Fig. 6C

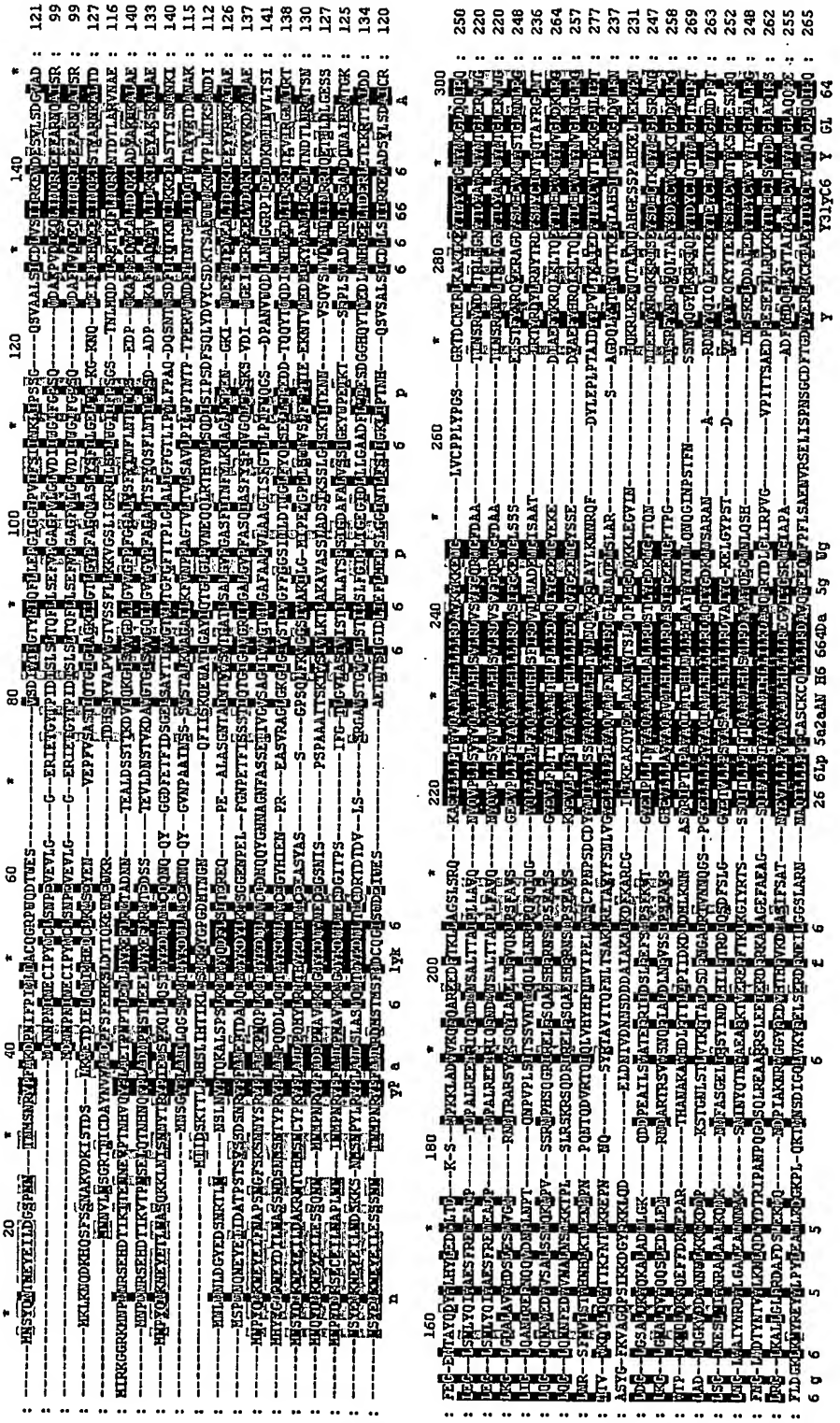

Fig. 7A

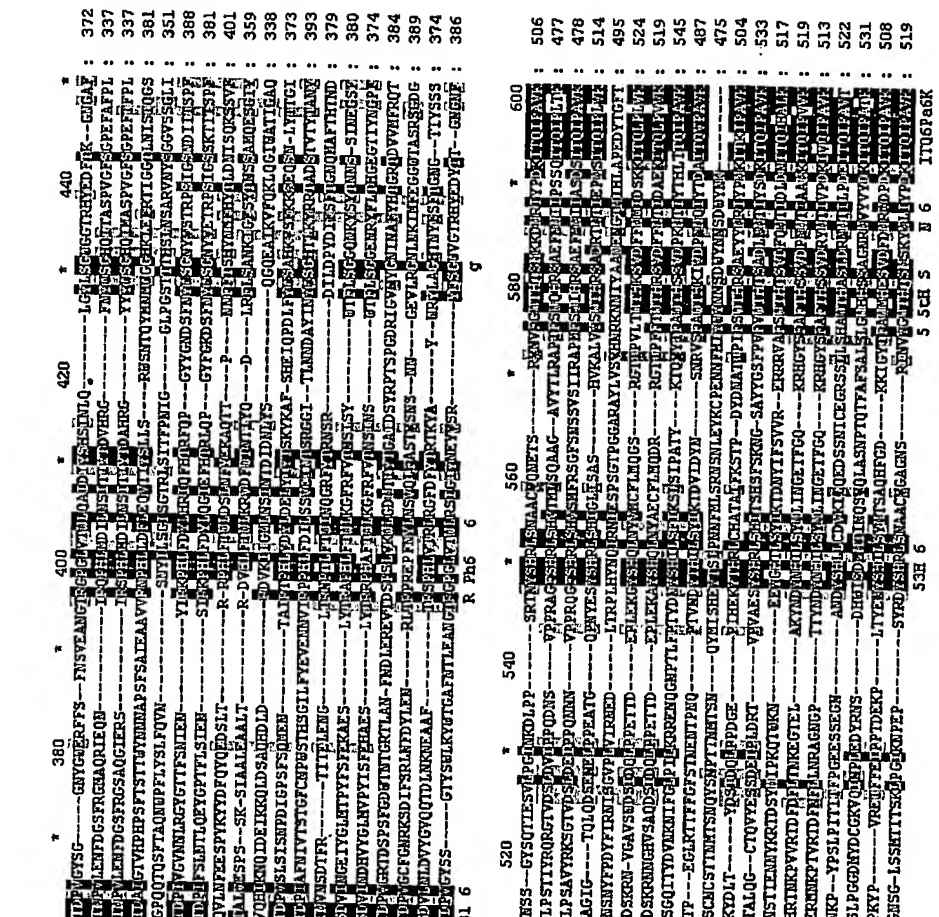

Fig. 7B

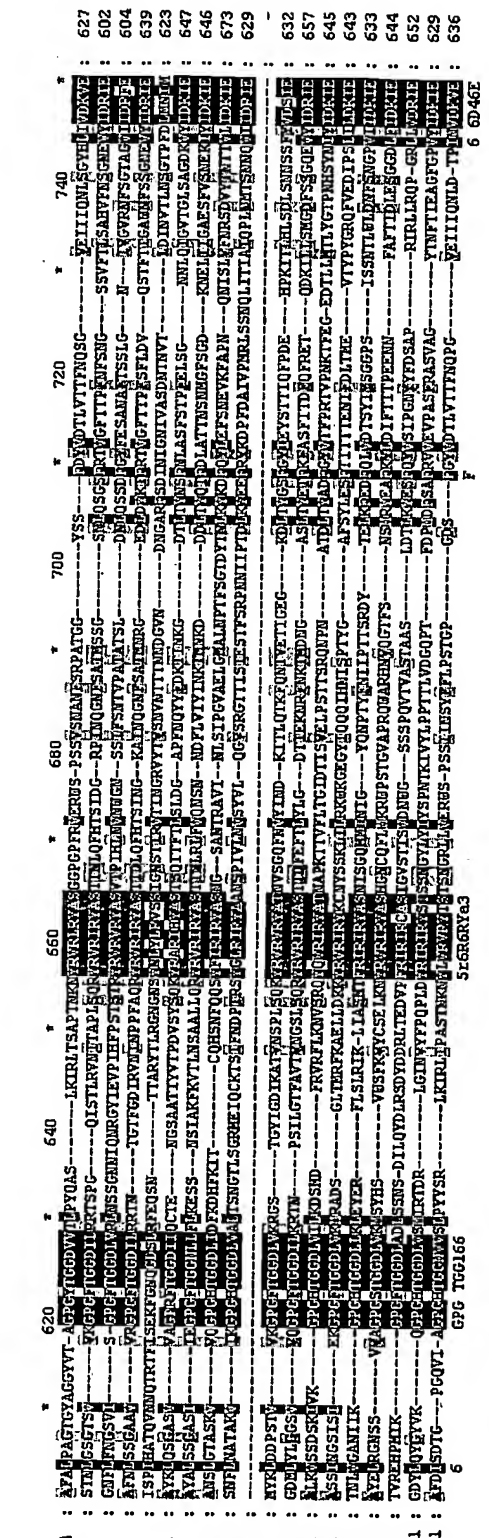

Fig. 7C

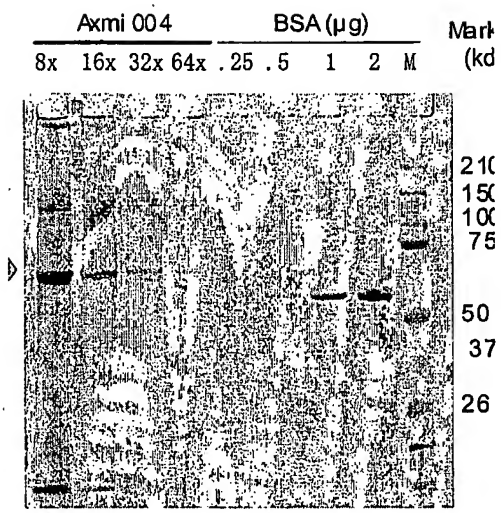
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Fig. 8

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Carr, Brian

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gaattagcag gtatacaaag aaaccttgaa acatatatac aattacgtaa tgaatgggaa 720
aatgatattg aaaactcaaa ggctcaaggt aaggtagcta attactatga aagtcttgag 780
caggcggttg aaaggagtat gcctcaattt gcagtggaga attttgaagt accactttta 840
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aatataagat cacctctata tggtagagag gcaaatcaag aggttcctag agatttttat 1440
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gcaccagctc ctccttttaa tttacgtagc ttagagggag tagaattcca cactcctaca 1560
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gctgaagaaa ccaatacaat tgaatcaaat attattacgc aaatcccgtt agtaaaagca 1800
tatcaaattg ggtcaggcac tactgtaagg aaaggaccag gattcacagg aggggatata 1860
cttcgaagaa caggtcctgg aacatttgga gatatgagaa taaatattaa tgcaccatta 1920
tctcaaagat atcgtgtaag gattcgttat gcttctacga cagatttaca atttgtcacg 1980
agtattaatg ggaccaccat taatattggt aacttcccga aaactattaa taatctaaat 2040
actttaggtt ctgagggcta tagaacagta tcgtttagta ctccatttag tttctcaaat 2100
gcacaaagca tatttagatt aggtatacaa gcattttctg gagttcaaga agtttatgtg 2160
gataaaattg aatttattcc tgttgaatag 2190

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<211> 1890
<212> DNA
<213> Bacillus thuringiensis

<220>
<221> CDS
<222> (1)...(1890)

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Met Ser Glu Leu Lys Gly Lys Phe Lys Lys Ser Thr Asn Arg Thr Cys
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tgt ttg cta aaa ata ata aat ata gga gga aga ggt atg aat tca aag 96
Cys Leu Leu Lys Ile Ile Asn Ile Gly Gly Arg Gly Met Asn Ser Lys
20 25 30

gaa cat gat tat cta aaa gtt tgt aat gat tta agt gac gcc aat att 144
Glu His Asp Tyr Leu Lys Val Cys Asn Asp Leu Ser Asp Ala Asn Ile
35 40 45

aat atg gaa cgg ttt gat aag aat gat gca ctg gaa att ggt atg tcc 192
Asn Met Glu Arg Phe Asp Lys Asn Asp Ala Leu Glu Ile Gly Met Ser
50 55 60

att gta tct gaa ctt att ggt atg att cca ggc gga aca gct ttg caa 240
Ile Val Ser Glu Leu Ile Gly Met Ile Pro Gly Gly Thr Ala Leu Gln
65 70 75 80

ttt gtg ttt aat caa ttg tgg tct cgt tta ggt gat tct gga tgg aat 288
Phe Val Phe Asn Gln Leu Trp Ser Arg Leu Gly Asp Ser Gly Trp Asn
85 90 95

gcg ttc atg gaa cat gtg gag gaa tta att gat act aaa ata gaa ggg 336
Ala Phe Met Glu His Val Glu Glu Leu Ile Asp Thr Lys Ile Glu Gly
100 105 110

tat gca aaa aat aaa gcc tta tct gaa tta gca ggt ata caa aga aac 384
Tyr Ala Lys Asn Lys Ala Leu Ser Glu Leu Ala Gly Ile Gln Arg Asn
115 120 125

ctt gaa aca tat ata caa tta cgt aat gaa tgg gaa aat gat att gaa 432
Leu Glu Thr Tyr Ile Gln Leu Arg Asn Glu Trp Glu Asn Asp Ile Glu
130 135 140

aac tca aag gct caa ggt aag gta gct aat tac tat gaa agt ctt gag 480
Asn Ser Lys Ala Gln Gly Lys Val Ala Asn Tyr Tyr Glu Ser Leu Glu
145 150 155 160

cag gcg gtt gaa agg agt atg cct caa ttt gca gtg gag aat ttt gaa 528
Gln Ala Val Glu Arg Ser Met Pro Gln Phe Ala Val Glu Asn Phe Glu
165 170 175

gta cca ctt tta act gtc tat gtg caa gct gct aat ctt cat tta tta 576

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Val Pro Leu Leu Thr Val Tyr Val Gln Ala Ala Asn Leu His Leu Leu
            180                 185                 190

tta tta aga gat gtt tca gtt tat gga aag tgt tgg gga tgg tcg gag   624
Leu Leu Arg Asp Val Ser Val Tyr Gly Lys Cys Trp Gly Trp Ser Glu
        195                 200                 205

cag aaa att aaa att tat tat gat aaa cag att aag tat acc cat gaa   672
Gln Lys Ile Lys Ile Tyr Tyr Asp Lys Gln Ile Lys Tyr Thr His Glu
    210                 215                 220

tac aca aat cat tgt gta aat tgg tat aat aaa gga ctt gag aga tta   720
Tyr Thr Asn His Cys Val Asn Trp Tyr Asn Lys Gly Leu Glu Arg Leu
225                 230                 235                 240

aaa aat aaa ggt tct tct tat caa gat tgg tac aat tat aat cgt ttc   768
Lys Asn Lys Gly Ser Ser Tyr Gln Asp Trp Tyr Asn Tyr Asn Arg Phe
                245                 250                 255

cgt aga gaa atg act ctt act gtt tta gat atc gtt gct tta ttc ccg   816
Arg Arg Glu Met Thr Leu Thr Val Leu Asp Ile Val Ala Leu Phe Pro
            260                 265                 270

cac tat gat gta caa act tat cca ata aca acc gtt gct cag cta aca   864
His Tyr Asp Val Gln Thr Tyr Pro Ile Thr Thr Val Ala Gln Leu Thr
        275                 280                 285

agg gaa gtt tat acg gat cct tta ctt aat ttt aat cct aaa tta cat   912
Arg Glu Val Tyr Thr Asp Pro Leu Leu Asn Phe Asn Pro Lys Leu His
    290                 295                 300

tct gtg tct caa tta cct agt ttt agt gac atg gaa aat gca aca att   960
Ser Val Ser Gln Leu Pro Ser Phe Ser Asp Met Glu Asn Ala Thr Ile
305                 310                 315                 320

aga act cca cat ctg atg gaa ttt tta aga atg cta aca att tat aca   1008
Arg Thr Pro His Leu Met Glu Phe Leu Arg Met Leu Thr Ile Tyr Thr
                325                 330                 335

gat tgg tat agt gtg gga aga aac tat tat tgg gga gga cat cgc gtg   1056
Asp Trp Tyr Ser Val Gly Arg Asn Tyr Tyr Trp Gly Gly His Arg Val
            340                 345                 350

acg tct tac cat gta gga gga gag aat ata aga tca cct cta tat ggt   1104
Thr Ser Tyr His Val Gly Gly Glu Asn Ile Arg Ser Pro Leu Tyr Gly
        355                 360                 365

aga gag gca aat caa gag gtt cct aga gat ttt tat ttt tat gga ccc   1152
Arg Glu Ala Asn Gln Glu Val Pro Arg Asp Phe Tyr Phe Tyr Gly Pro
    370                 375                 380

gtt ttt aag acg tta tca aag ccg act cta aga cca tta cag cag cct   1200
Val Phe Lys Thr Leu Ser Lys Pro Thr Leu Arg Pro Leu Gln Gln Pro
385                 390                 395                 400

gca cca gct cct cct ttt aat tta cgt agc tta gag gga gta gaa ttc   1248
Ala Pro Ala Pro Pro Phe Asn Leu Arg Ser Leu Glu Gly Val Glu Phe
                405                 410                 415

cac act cct aca ggt agt ttt atg tat cgt gaa aga gga tcg gta gat   1296
His Thr Pro Thr Gly Ser Phe Met Tyr Arg Glu Arg Gly Ser Val Asp
            420                 425                 430

tct ttt aat gag ttg ccg cct ttt aat cca gtt ggg tta cct cat aag   1344
Ser Phe Asn Glu Leu Pro Pro Phe Asn Pro Val Gly Leu Pro His Lys
        435                 440                 445

gta tac agt cac cgt tta tgt cat gca acg ttt gtt cgt aaa tct ggg   1392
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Val Tyr Ser His Arg Leu Cys His Ala Thr Phe Val Arg Lys Ser Gly
    450                 455                 460

acc cct tat tta aca aca ggt gcc atc ttt tct tgg aca cat cgt agt   1440
Thr Pro Tyr Leu Thr Thr Gly Ala Ile Phe Ser Trp Thr His Arg Ser
465                 470                 475                 480

gct gaa gaa acc aat aca att gaa tca aat att att acg caa atc ccg   1488
Ala Glu Glu Thr Asn Thr Ile Glu Ser Asn Ile Ile Thr Gln Ile Pro
                485                 490                 495

tta gta aaa gca tat caa att ggg tca ggc act act gta agg aaa gga   1536
Leu Val Lys Ala Tyr Gln Ile Gly Ser Gly Thr Thr Val Arg Lys Gly
            500                 505                 510

cca gga ttc aca gga ggg gat ata ctt cga aga aca ggt cct gga aca   1584
Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Gly Pro Gly Thr
        515                 520                 525

ttt gga gat atg aga ata aat att aat gca cca tta tct caa aga tat   1632
Phe Gly Asp Met Arg Ile Asn Ile Asn Ala Pro Leu Ser Gln Arg Tyr
    530                 535                 540

cgt gta agg att cgt tat gct tct acg aca gat tta caa ttt gtc acg   1680
Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe Val Thr
545                 550                 555                 560

agt att aat ggg acc acc att aat att ggt aac ttc ccg aaa act att   1728
Ser Ile Asn Gly Thr Thr Ile Asn Ile Gly Asn Phe Pro Lys Thr Ile
                565                 570                 575

aat aat cta aat act tta ggt tct gag ggc tat aga aca gta tcg ttt   1776
Asn Asn Leu Asn Thr Leu Gly Ser Glu Gly Tyr Arg Thr Val Ser Phe
            580                 585                 590

agt act cca ttt agt ttc tca aat gca caa agc ata ttt aga tta ggt   1824
Ser Thr Pro Phe Ser Phe Ser Asn Ala Gln Ser Ile Phe Arg Leu Gly
        595                 600                 605

ata caa gca ttt tct gga gtt caa gaa gtt tat gtg gat aaa att gaa   1872
Ile Gln Ala Phe Ser Gly Val Gln Glu Val Tyr Val Asp Lys Ile Glu
    610                 615                 620

ttt att cct gtt gaa tag                                          1890
Phe Ile Pro Val Glu  *
625


<210> 3
<211> 629
<212> PRT
<213> Bacillus thuringiensis

<400> 3
Met Ser Glu Leu Lys Gly Lys Phe Lys Lys Ser Thr Asn Arg Thr Cys
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Cys Leu Leu Lys Ile Ile Asn Ile Gly Gly Arg Gly Met Asn Ser Lys
            20                  25                  30
Glu His Asp Tyr Leu Lys Val Cys Asn Asp Leu Ser Asp Ala Asn Ile
        35                  40                  45
Asn Met Glu Arg Phe Asp Lys Asn Asp Ala Leu Glu Ile Gly Met Ser
    50                  55                  60
Ile Val Ser Glu Leu Ile Gly Met Ile Pro Gly Gly Thr Ala Leu Gln
65                  70                  75                  80
Phe Val Phe Asn Gln Leu Trp Ser Arg Leu Gly Asp Ser Gly Trp Asn
                85                  90                  95
Ala Phe Met Glu His Val Glu Glu Leu Ile Asp Thr Lys Ile Glu Gly
            100                 105                 110
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Tyr Ala Lys Asn Lys Ala Leu Ser Glu Leu Ala Gly Ile Gln Arg Asn
        115                 120                 125
Leu Glu Thr Tyr Ile Gln Leu Arg Asn Glu Trp Glu Asn Asp Ile Glu
    130                 135                 140
Asn Ser Lys Ala Gln Gly Lys Val Ala Asn Tyr Tyr Glu Ser Leu Glu
145                 150                 155                 160
Gln Ala Val Glu Arg Ser Met Pro Gln Phe Ala Val Glu Asn Phe Glu
                165                 170                 175
Val Pro Leu Leu Thr Val Tyr Val Gln Ala Ala Asn Leu His Leu Leu
            180                 185                 190
Leu Leu Arg Asp Val Ser Val Tyr Gly Lys Cys Trp Gly Trp Ser Glu
        195                 200                 205
Gln Lys Ile Lys Ile Tyr Tyr Asp Lys Gln Ile Lys Tyr Thr His Glu
    210                 215                 220
Tyr Thr Asn His Cys Val Asn Trp Tyr Asn Lys Gly Leu Glu Arg Leu
225                 230                 235                 240
Lys Asn Lys Gly Ser Ser Tyr Gln Asp Trp Tyr Asn Tyr Asn Arg Phe
                245                 250                 255
Arg Arg Glu Met Thr Leu Thr Val Leu Asp Ile Val Ala Leu Phe Pro
            260                 265                 270
His Tyr Asp Val Gln Thr Tyr Pro Ile Thr Thr Val Ala Gln Leu Thr
        275                 280                 285
Arg Glu Val Tyr Thr Asp Pro Leu Leu Asn Phe Asn Pro Lys Leu His
    290                 295                 300
Ser Val Ser Gln Leu Pro Ser Phe Ser Asp Met Glu Asn Ala Thr Ile
305                 310                 315                 320
Arg Thr Pro His Leu Met Glu Phe Leu Arg Met Leu Thr Ile Tyr Thr
                325                 330                 335
Asp Trp Tyr Ser Val Gly Arg Asn Tyr Tyr Trp Gly Gly His Arg Val
            340                 345                 350
Thr Ser Tyr His Val Gly Gly Glu Asn Ile Arg Ser Pro Leu Tyr Gly
        355                 360                 365
Arg Glu Ala Asn Gln Glu Val Pro Arg Asp Phe Tyr Phe Tyr Gly Pro
    370                 375                 380
Val Phe Lys Thr Leu Ser Lys Pro Thr Leu Arg Pro Leu Gln Gln Pro
385                 390                 395                 400
Ala Pro Ala Pro Pro Phe Asn Leu Arg Ser Leu Glu Gly Val Glu Phe
                405                 410                 415
His Thr Pro Thr Gly Ser Phe Met Tyr Arg Glu Arg Gly Ser Val Asp
            420                 425                 430
Ser Phe Asn Glu Leu Pro Pro Phe Asn Pro Val Gly Leu Pro His Lys
        435                 440                 445
Val Tyr Ser His Arg Leu Cys His Ala Thr Phe Val Arg Lys Ser Gly
    450                 455                 460
Thr Pro Tyr Leu Thr Thr Gly Ala Ile Phe Ser Trp Thr His Arg Ser
465                 470                 475                 480
Ala Glu Glu Thr Asn Thr Ile Glu Ser Asn Ile Ile Thr Gln Ile Pro
                485                 490                 495
Leu Val Lys Ala Tyr Gln Ile Gly Ser Gly Thr Thr Val Arg Lys Gly
            500                 505                 510
Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Gly Pro Gly Thr
        515                 520                 525
Phe Gly Asp Met Arg Ile Asn Ile Asn Ala Pro Leu Ser Gln Arg Tyr
    530                 535                 540
Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe Val Thr
545                 550                 555                 560
Ser Ile Asn Gly Thr Thr Ile Asn Ile Gly Asn Phe Pro Lys Thr Ile
                565                 570                 575
Asn Asn Leu Asn Thr Leu Gly Ser Glu Gly Tyr Arg Thr Val Ser Phe
            580                 585                 590
Ser Thr Pro Phe Ser Phe Ser Asn Ala Gln Ser Ile Phe Arg Leu Gly
        595                 600                 605
Ile Gln Ala Phe Ser Gly Val Gln Glu Val Tyr Val Asp Lys Ile Glu
    610                 615                 620
Phe Ile Pro Val Glu
625
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<210> 4
<211> 1806
<212> DNA
<213> Bacillus thuringiensis

<220>
<221> CDS
<222> (1)...(1806)

<400> 4

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atg aat tca aag gaa cat gat tat cta aaa gtt tgt aat gat tta agt   48
Met Asn Ser Lys Glu His Asp Tyr Leu Lys Val Cys Asn Asp Leu Ser
 1               5                  10                  15

gac gcc aat att aat atg gaa cgg ttt gat aag aat gat gca ctg gaa   96
Asp Ala Asn Ile Asn Met Glu Arg Phe Asp Lys Asn Asp Ala Leu Glu
            20                  25                  30

att ggt atg tcc att gta tct gaa ctt att ggt atg att cca ggc gga   144
Ile Gly Met Ser Ile Val Ser Glu Leu Ile Gly Met Ile Pro Gly Gly
        35                  40                  45

aca gct ttg caa ttt gtg ttt aat caa ttg tgg tct cgt tta ggt gat   192
Thr Ala Leu Gln Phe Val Phe Asn Gln Leu Trp Ser Arg Leu Gly Asp
    50                  55                  60

tct gga tgg aat gcg ttc atg gaa cat gtg gag gaa tta att gat act   240
Ser Gly Trp Asn Ala Phe Met Glu His Val Glu Glu Leu Ile Asp Thr
65                  70                  75                  80

aaa ata gaa ggg tat gca aaa aat aaa gcc tta tct gaa tta gca ggt   288
Lys Ile Glu Gly Tyr Ala Lys Asn Lys Ala Leu Ser Glu Leu Ala Gly
                85                  90                  95

ata caa aga aac ctt gaa aca tat ata caa tta cgt aat gaa tgg gaa   336
Ile Gln Arg Asn Leu Glu Thr Tyr Ile Gln Leu Arg Asn Glu Trp Glu
            100                 105                 110

aat gat att gaa aac tca aag gct caa ggt aag gta gct aat tac tat   384
Asn Asp Ile Glu Asn Ser Lys Ala Gln Gly Lys Val Ala Asn Tyr Tyr
        115                 120                 125

gaa agt ctt gag cag gcg gtt gaa agg agt atg cct caa ttt gca gtg   432
Glu Ser Leu Glu Gln Ala Val Glu Arg Ser Met Pro Gln Phe Ala Val
    130                 135                 140

gag aat ttt gaa gta cca ctt tta act gtc tat gtg caa gct gct aat   480
Glu Asn Phe Glu Val Pro Leu Leu Thr Val Tyr Val Gln Ala Ala Asn
145                 150                 155                 160

ctt cat tta tta tta tta aga gat gtt tca gtt tat gga aag tgt tgg   528
Leu His Leu Leu Leu Leu Arg Asp Val Ser Val Tyr Gly Lys Cys Trp
                165                 170                 175

gga tgg tcg gag cag aaa att aaa att tat tat gat aaa cag att aag   576
Gly Trp Ser Glu Gln Lys Ile Lys Ile Tyr Tyr Asp Lys Gln Ile Lys
            180                 185                 190

tat acc cat gaa tac aca aat cat tgt gta aat tgg tat aat aaa gga   624
Tyr Thr His Glu Tyr Thr Asn His Cys Val Asn Trp Tyr Asn Lys Gly
        195                 200                 205

ctt gag aga tta aaa aat aaa ggt tct tct tat caa gat tgg tac aat   672
Leu Glu Arg Leu Lys Asn Lys Gly Ser Ser Tyr Gln Asp Trp Tyr Asn
    210                 215                 220

tat aat cgt ttc cgt aga gaa atg act ctt act gtt tta gat atc gtt   720
Tyr Asn Arg Phe Arg Arg Glu Met Thr Leu Thr Val Leu Asp Ile Val
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225                 230                 235                 240

gct tta ttc ccg cac tat gat gta caa act tat cca ata aca acc gtt   768
Ala Leu Phe Pro His Tyr Asp Val Gln Thr Tyr Pro Ile Thr Thr Val
                245                 250                 255

gct cag cta aca agg gaa gtt tat acg gat cct tta ctt aat ttt aat   816
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Leu Asn Phe Asn
            260                 265                 270

cct aaa tta cat tct gtg tct caa tta cct agt ttt agt gac atg gaa   864
Pro Lys Leu His Ser Val Ser Gln Leu Pro Ser Phe Ser Asp Met Glu
        275                 280                 285

aat gca aca att aga act cca cat ctg atg gaa ttt tta aga atg cta   912
Asn Ala Thr Ile Arg Thr Pro His Leu Met Glu Phe Leu Arg Met Leu
    290                 295                 300

aca att tat aca gat tgg tat agt gtg gga aga aac tat tat tgg gga   960
Thr Ile Tyr Thr Asp Trp Tyr Ser Val Gly Arg Asn Tyr Tyr Trp Gly
305                 310                 315                 320

gga cat cgc gtg acg tct tac cat gta gga gga gag aat ata aga tca   1008
Gly His Arg Val Thr Ser Tyr His Val Gly Gly Glu Asn Ile Arg Ser
                325                 330                 335

cct cta tat ggt aga gag gca aat caa gag gtt cct aga gat ttt tat   1056
Pro Leu Tyr Gly Arg Glu Ala Asn Gln Glu Val Pro Arg Asp Phe Tyr
            340                 345                 350

ttt tat gga ccc gtt ttt aag acg tta tca aag ccg act cta aga cca   1104
Phe Tyr Gly Pro Val Phe Lys Thr Leu Ser Lys Pro Thr Leu Arg Pro
        355                 360                 365

tta cag cag cct gca cca gct cct cct ttt aat tta cgt agc tta gag   1152
Leu Gln Gln Pro Ala Pro Ala Pro Pro Phe Asn Leu Arg Ser Leu Glu
    370                 375                 380

gga gta gaa ttc cac act cct aca ggt agt ttt atg tat cgt gaa aga   1200
Gly Val Glu Phe His Thr Pro Thr Gly Ser Phe Met Tyr Arg Glu Arg
385                 390                 395                 400

gga tcg gta gat tct ttt aat gag ttg ccg cct ttt aat cca gtt ggg   1248
Gly Ser Val Asp Ser Phe Asn Glu Leu Pro Pro Phe Asn Pro Val Gly
                405                 410                 415

tta cct cat aag gta tac agt cac cgt tta tgt cat gca acg ttt gtt   1296
Leu Pro His Lys Val Tyr Ser His Arg Leu Cys His Ala Thr Phe Val
            420                 425                 430

cgt aaa tct ggg acc cct tat tta aca aca ggt gcc atc ttt tct tgg   1344
Arg Lys Ser Gly Thr Pro Tyr Leu Thr Thr Gly Ala Ile Phe Ser Trp
        435                 440                 445

aca cat cgt agt gct gaa gaa acc aat aca att gaa tca aat att att   1392
Thr His Arg Ser Ala Glu Glu Thr Asn Thr Ile Glu Ser Asn Ile Ile
    450                 455                 460

acg caa atc ccg tta gta aaa gca tat caa att ggg tca ggc act act   1440
Thr Gln Ile Pro Leu Val Lys Ala Tyr Gln Ile Gly Ser Gly Thr Thr
465                 470                 475                 480

gta agg aaa gga cca gga ttc aca gga ggg gat ata ctt cga aga aca   1488
Val Arg Lys Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr
                485                 490                 495

ggt cct gga aca ttt gga gat atg aga ata aat att aat gca cca tta   1536
Gly Pro Gly Thr Phe Gly Asp Met Arg Ile Asn Ile Asn Ala Pro Leu
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            500                 505                 510

tct caa aga tat cgt gta agg att cgt tat gct tct acg aca gat tta   1584
Ser Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu
        515                 520                 525

caa ttt gtc acg agt att aat ggg acc acc att aat att ggt aac ttc   1632
Gln Phe Val Thr Ser Ile Asn Gly Thr Thr Ile Asn Ile Gly Asn Phe
    530                 535                 540

ccg aaa act att aat aat cta aat act tta ggt tct gag ggc tat aga   1680
Pro Lys Thr Ile Asn Asn Leu Asn Thr Leu Gly Ser Glu Gly Tyr Arg
545                 550                 555                 560

aca gta tcg ttt agt act cca ttt agt ttc tca aat gca caa agc ata   1728
Thr Val Ser Phe Ser Thr Pro Phe Ser Phe Ser Asn Ala Gln Ser Ile
                565                 570                 575

ttt aga tta ggt ata caa gca ttt tct gga gtt caa gaa gtt tat gtg   1776
Phe Arg Leu Gly Ile Gln Ala Phe Ser Gly Val Gln Glu Val Tyr Val
            580                 585                 590

gat aaa att gaa ttt att cct gtt gaa tag                          1806
Asp Lys Ile Glu Phe Ile Pro Val Glu  *
        595                 600
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<210> 5
<211> 601
<212> PRT
<213> Bacillus thuringiensis

<400> 5

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Met Asn Ser Lys Glu His Asp Tyr Leu Lys Val Cys Asn Asp Leu Ser
 1               5                  10                  15
Asp Ala Asn Ile Asn Met Glu Arg Phe Asp Lys Asn Asp Ala Leu Glu
            20                  25                  30
Ile Gly Met Ser Ile Val Ser Glu Leu Ile Gly Met Ile Pro Gly Gly
        35                  40                  45
Thr Ala Leu Gln Phe Val Phe Asn Gln Leu Trp Ser Arg Leu Gly Asp
    50                  55                  60
Ser Gly Trp Asn Ala Phe Met Glu His Val Glu Glu Leu Ile Asp Thr
65                  70                  75                  80
Lys Ile Glu Gly Tyr Ala Lys Asn Lys Ala Leu Ser Glu Leu Ala Gly
                85                  90                  95
Ile Gln Arg Asn Leu Glu Thr Tyr Ile Gln Leu Arg Asn Glu Trp Glu
            100                 105                 110
Asn Asp Ile Glu Asn Ser Lys Ala Gln Gly Lys Val Ala Asn Tyr Tyr
        115                 120                 125
Glu Ser Leu Glu Gln Ala Val Glu Arg Ser Met Pro Gln Phe Ala Val
    130                 135                 140
Glu Asn Phe Glu Val Pro Leu Leu Thr Val Tyr Val Gln Ala Ala Asn
145                 150                 155                 160
Leu His Leu Leu Leu Leu Arg Asp Val Ser Val Tyr Gly Lys Cys Trp
                165                 170                 175
Gly Trp Ser Glu Gln Lys Ile Lys Ile Tyr Tyr Asp Lys Gln Ile Lys
            180                 185                 190
Tyr Thr His Glu Tyr Thr Asn His Cys Val Asn Trp Tyr Asn Lys Gly
        195                 200                 205
Leu Glu Arg Leu Lys Asn Lys Gly Ser Ser Tyr Gln Asp Trp Tyr Asn
    210                 215                 220
Tyr Asn Arg Phe Arg Arg Glu Met Thr Leu Thr Val Leu Asp Ile Val
225                 230                 235                 240
Ala Leu Phe Pro His Tyr Asp Val Gln Thr Tyr Pro Ile Thr Thr Val
                245                 250                 255
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Leu Asn Phe Asn
            260                 265                 270
Pro Lys Leu His Ser Val Ser Gln Leu Pro Ser Phe Ser Asp Met Glu
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        275                 280                 285
Asn Ala Thr Ile Arg Thr Pro His Leu Met Glu Phe Leu Arg Met Leu
    290                 295                 300
Thr Ile Tyr Thr Asp Trp Tyr Ser Val Gly Arg Asn Tyr Tyr Trp Gly
305                 310                 315                 320
Gly His Arg Val Thr Ser Tyr His Val Gly Gly Glu Asn Ile Arg Ser
                325                 330                 335
Pro Leu Tyr Gly Arg Glu Ala Asn Gln Glu Val Pro Arg Asp Phe Tyr
            340                 345                 350
Phe Tyr Gly Pro Val Phe Lys Thr Leu Ser Lys Pro Thr Leu Arg Pro
        355                 360                 365
Leu Gln Gln Pro Ala Pro Ala Pro Pro Phe Asn Leu Arg Ser Leu Glu
    370                 375                 380
Gly Val Glu Phe His Thr Pro Thr Gly Ser Phe Met Tyr Arg Glu Arg
385                 390                 395                 400
Gly Ser Val Asp Ser Phe Asn Glu Leu Pro Pro Phe Asn Pro Val Gly
                405                 410                 415
Leu Pro His Lys Val Tyr Ser His Arg Leu Cys His Ala Thr Phe Val
            420                 425                 430
Arg Lys Ser Gly Thr Pro Tyr Leu Thr Thr Gly Ala Ile Phe Ser Trp
        435                 440                 445
Thr His Arg Ser Ala Glu Glu Thr Asn Thr Ile Glu Ser Asn Ile Ile
    450                 455                 460
Thr Gln Ile Pro Leu Val Lys Ala Tyr Gln Ile Gly Ser Gly Thr Thr
465                 470                 475                 480
Val Arg Lys Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr
                485                 490                 495
Gly Pro Gly Thr Phe Gly Asp Met Arg Ile Asn Ile Asn Ala Pro Leu
            500                 505                 510
Ser Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu
        515                 520                 525
Gln Phe Val Thr Ser Ile Asn Gly Thr Thr Ile Asn Ile Gly Asn Phe
    530                 535                 540
Pro Lys Thr Ile Asn Asn Leu Asn Thr Leu Gly Ser Glu Gly Tyr Arg
545                 550                 555                 560
Thr Val Ser Phe Ser Thr Pro Phe Ser Phe Ser Asn Ala Gln Ser Ile
                565                 570                 575
Phe Arg Leu Gly Ile Gln Ala Phe Ser Gly Val Gln Glu Val Tyr Val
            580                 585                 590
Asp Lys Ile Glu Phe Ile Pro Val Glu
        595                 600
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<210> 6
<211> 2208
<212> DNA
<213> Bacillus thuringiensis

<220>
<221> CDS
<222> (1)...(2208)

<400> 6

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atg aat caa aat aac gat aat aac gaa tat gaa att att gat tcg cat   48
Met Asn Gln Asn Asn Asp Asn Asn Glu Tyr Glu Ile Ile Asp Ser His
 1               5                  10                  15

acc tca cct tat ttt ccg aac aga aac agt aat gat tct aga tac cct   96
Thr Ser Pro Tyr Phe Pro Asn Arg Asn Ser Asn Asp Ser Arg Tyr Pro
             20                  25                  30

tac aca aat aat cca aat caa cca tta caa aac aca aat tac aaa gag   144
Tyr Thr Asn Asn Pro Asn Gln Pro Leu Gln Asn Thr Asn Tyr Lys Glu
         35                  40                  45

tgg ctc aat atg tgt caa ggg aat aca caa tat ggt gat aat ttc gag   192
Trp Leu Asn Met Cys Gln Gly Asn Thr Gln Tyr Gly Asp Asn Phe Glu
     50                  55                  60
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aca ttt gct agt gct gat aca att gct gca gtt agt gca ggt act att   240
Thr Phe Ala Ser Ala Asp Thr Ile Ala Ala Val Ser Ala Gly Thr Ile
 65                  70                  75                  80

gta tcc ggt act ctg tta gcc ggt ata ggt ggg ctc act tct ata tcc   288
Val Ser Gly Thr Leu Leu Ala Gly Ile Gly Gly Leu Thr Ser Ile Ser
                85                  90                  95

gga ccg ata gga ata ata ggt gct ata ata ata tct ttt ggt acc cta   336
Gly Pro Ile Gly Ile Ile Gly Ala Ile Ile Ile Ser Phe Gly Thr Leu
            100                 105                 110

atc act gtc ttt tgg ccc gcg gga gaa caa gac aaa aca gta tgg aca   384
Ile Thr Val Phe Trp Pro Ala Gly Glu Gln Asp Lys Thr Val Trp Thr
        115                 120                 125

caa ttt att aaa atg gga gaa att ttt gtt gat aca ccg tta aca gaa   432
Gln Phe Ile Lys Met Gly Glu Ile Phe Val Asp Thr Pro Leu Thr Glu
    130                 135                 140

agc ata aaa cag cta aag tta caa act tta gaa gga ttt aga caa ata   480
Ser Ile Lys Gln Leu Lys Leu Gln Thr Leu Glu Gly Phe Arg Gln Ile
145                 150                 155                 160

tta caa agc tat aat aca gca tta gat gat tgg aga aaa tta aaa aga   528
Leu Gln Ser Tyr Asn Thr Ala Leu Asp Asp Trp Arg Lys Leu Lys Arg
                165                 170                 175

cta caa gct cct gga tta cca cca tca tca gca tta caa caa gct gcc   576
Leu Gln Ala Pro Gly Leu Pro Pro Ser Ser Ala Leu Gln Gln Ala Ala
            180                 185                 190

ttg act ctt aaa ata cga ttt gag aat gtt cac aat gat ttt att cga   624
Leu Thr Leu Lys Ile Arg Phe Glu Asn Val His Asn Asp Phe Ile Arg
        195                 200                 205

gaa ata cct ggt ttc caa ctt gaa act tat aaa acg cta tta cta cct   672
Glu Ile Pro Gly Phe Gln Leu Glu Thr Tyr Lys Thr Leu Leu Leu Pro
    210                 215                 220

att tat gcg caa gct gct aat ttt cat tta aat tta tta caa caa ggt   720
Ile Tyr Ala Gln Ala Ala Asn Phe His Leu Asn Leu Leu Gln Gln Gly
225                 230                 235                 240

gct gaa ttg gct gat gaa tgg aat gca gat ata cat cct tca caa att   768
Ala Glu Leu Ala Asp Glu Trp Asn Ala Asp Ile His Pro Ser Gln Ile
                245                 250                 255

gaa cct aat gct gga aca tca gat gac tat tat aaa ctt tta aaa gaa   816
Glu Pro Asn Ala Gly Thr Ser Asp Asp Tyr Tyr Lys Leu Leu Lys Glu
            260                 265                 270

aat ata cct aaa tat agt aac tat tgt gca aat acc tat aga aca gga   864
Asn Ile Pro Lys Tyr Ser Asn Tyr Cys Ala Asn Thr Tyr Arg Thr Gly
        275                 280                 285

cta aaa aat ctt aga gac gaa cca aat atg aaa tgg agt ata ttt aat   912
Leu Lys Asn Leu Arg Asp Glu Pro Asn Met Lys Trp Ser Ile Phe Asn
    290                 295                 300

gac tat cga aga tat atg acc att act gta tta gat acc atc tct caa   960
Asp Tyr Arg Arg Tyr Met Thr Ile Thr Val Leu Asp Thr Ile Ser Gln
305                 310                 315                 320

ttt tct tta tat gat ata aaa aga tat aga gat tca ata gga gga ata  1008
Phe Ser Leu Tyr Asp Ile Lys Arg Tyr Arg Asp Ser Ile Gly Gly Ile
                325                 330                 335
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gaa gta aaa ggc att aag aat gaa ctc aca aga gaa att tat aca act   1056
Glu Val Lys Gly Ile Lys Asn Glu Leu Thr Arg Glu Ile Tyr Thr Thr
            340                 345                 350

gaa ata aat ttt gat cgt ctt cct caa ctt aga gtt caa ccc aat cta   1104
Glu Ile Asn Phe Asp Arg Leu Pro Gln Leu Arg Val Gln Pro Asn Leu
        355                 360                 365

gct acg atg gaa tat aat tta aca cgt gca agt ttt aaa tta ttt tca   1152
Ala Thr Met Glu Tyr Asn Leu Thr Arg Ala Ser Phe Lys Leu Phe Ser
    370                 375                 380

ttt tta gaa caa ttt att ttt tat aca gaa aat aca aat ttc ggg aat   1200
Phe Leu Glu Gln Phe Ile Phe Tyr Thr Glu Asn Thr Asn Phe Gly Asn
385                 390                 395                 400

cgt tta gtt ggt att tct aat cgt gat gca cct act tat agc aat act   1248
Arg Leu Val Gly Ile Ser Asn Arg Asp Ala Pro Thr Tyr Ser Asn Thr
                405                 410                 415

ata act gaa act tta tat gga gaa aga aca ggt tca ccc aca aca aaa   1296
Ile Thr Glu Thr Leu Tyr Gly Glu Arg Thr Gly Ser Pro Thr Thr Lys
            420                 425                 430

aca ata aga cca ttt gaa tct tat aaa gtt tca att gta act gat aga   1344
Thr Ile Arg Pro Phe Glu Ser Tyr Lys Val Ser Ile Val Thr Asp Arg
        435                 440                 445

caa tca cct cct gtt tcc cct att caa cca cac ttt ata att aat caa   1392
Gln Ser Pro Pro Val Ser Pro Ile Gln Pro His Phe Ile Ile Asn Gln
    450                 455                 460

att gaa ctt tat tta aat ggc tca tct aac aac aca ctc aaa tat tca   1440
Ile Glu Leu Tyr Leu Asn Gly Ser Ser Asn Asn Thr Leu Lys Tyr Ser
465                 470                 475                 480

gca gga ggg tct tta tct aat tat caa aac aca act ttt ttt caa ttt   1488
Ala Gly Gly Ser Leu Ser Asn Tyr Gln Asn Thr Thr Phe Phe Gln Phe
                485                 490                 495

cct aga aaa aaa gac tgc aat cta gtt att gat cca ggt tgt tca cca   1536
Pro Arg Lys Lys Asp Cys Asn Leu Val Ile Asp Pro Gly Cys Ser Pro
            500                 505                 510

aac ttt aat aac tat agt cat att tta tcc cat ttt tca tta ttt act   1584
Asn Phe Asn Asn Tyr Ser His Ile Leu Ser His Phe Ser Leu Phe Thr
        515                 520                 525

tat tcc tat gtg att gga tta cag cta caa ata tta gat aca ggt gta   1632
Tyr Ser Tyr Val Ile Gly Leu Gln Leu Gln Ile Leu Asp Thr Gly Val
    530                 535                 540

tta gga tgg aca cac agt agt gtt gat aga tat aat gca ata tca gat   1680
Leu Gly Trp Thr His Ser Ser Val Asp Arg Tyr Asn Ala Ile Ser Asp
545                 550                 555                 560

aaa ata att aca atg atc cca gca atc aaa ggt aac aat ctt gat aca   1728
Lys Ile Ile Thr Met Ile Pro Ala Ile Lys Gly Asn Asn Leu Asp Thr
                565                 570                 575

aac tct aag gta att gaa gga cct ggt cat aca gga gga aac ttg gtt   1776
Asn Ser Lys Val Ile Glu Gly Pro Gly His Thr Gly Gly Asn Leu Val
            580                 585                 590

tat tta caa agt caa ggg cgt tta gaa att aca tgt gaa act cct aat   1824
Tyr Leu Gln Ser Gln Gly Arg Leu Glu Ile Thr Cys Glu Thr Pro Asn
        595                 600                 605
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tct aca caa tct tat ttc att aga ctt cga tat gct aca aat ggt gct   1872
Ser Thr Gln Ser Tyr Phe Ile Arg Leu Arg Tyr Ala Thr Asn Gly Ala
    610                 615                 620

gga aat act ctt cct aat ata tct ctt aca ata cca gga gta ata gga   1920
Gly Asn Thr Leu Pro Asn Ile Ser Leu Thr Ile Pro Gly Val Ile Gly
625                 630                 635                 640

ata cca cct caa cga ctc aac aac act ttt tct ggt aca aat tat aat   1968
Ile Pro Pro Gln Arg Leu Asn Asn Thr Phe Ser Gly Thr Asn Tyr Asn
                645                 650                 655

aat tta caa tac gga gat ttt ggg tat ttc caa ttt cca agt aca gta   2016
Asn Leu Gln Tyr Gly Asp Phe Gly Tyr Phe Gln Phe Pro Ser Thr Val
            660                 665                 670

aca tta cct tta aat cga aac ata cca ttt ata ttt aat cgt gca gat   2064
Thr Leu Pro Leu Asn Arg Asn Ile Pro Phe Ile Phe Asn Arg Ala Asp
        675                 680                 685

gta tca aat tca att tta atc att gat aaa att gaa ttt ata cca att   2112
Val Ser Asn Ser Ile Leu Ile Ile Asp Lys Ile Glu Phe Ile Pro Ile
    690                 695                 700

act tcc tct atg cac caa aat aga gaa aaa caa aaa tta gaa act atc   2160
Thr Ser Ser Met His Gln Asn Arg Glu Lys Gln Lys Leu Glu Thr Ile
705                 710                 715                 720

caa aca aaa ata aat aca ttt ttc aca aat cat aca aaa aca ctt tga   2208
Gln Thr Lys Ile Asn Thr Phe Phe Thr Asn His Thr Lys Thr Leu  *
                725                 730                 735
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<210> 7
<211> 735
<212> PRT
<213> Bacillus thuringiensis

<400> 7

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Met Asn Gln Asn Asn Asp Asn Asn Glu Tyr Glu Ile Ile Asp Ser His
 1               5                  10                  15
Thr Ser Pro Tyr Phe Pro Asn Arg Asn Ser Asn Asp Ser Arg Tyr Pro
            20                  25                  30
Tyr Thr Asn Asn Pro Asn Gln Pro Leu Gln Asn Thr Asn Tyr Lys Glu
        35                  40                  45
Trp Leu Asn Met Cys Gln Gly Asn Thr Gln Tyr Gly Asp Asn Phe Glu
    50                  55                  60
Thr Phe Ala Ser Ala Asp Thr Ile Ala Ala Val Ser Ala Gly Thr Ile
65                  70                  75                  80
Val Ser Gly Thr Leu Leu Ala Gly Ile Gly Gly Leu Thr Ser Ile Ser
                85                  90                  95
Gly Pro Ile Gly Ile Ile Gly Ala Ile Ile Ile Ser Phe Gly Thr Leu
            100                 105                 110
Ile Thr Val Phe Trp Pro Ala Gly Glu Gln Asp Lys Thr Val Trp Thr
        115                 120                 125
Gln Phe Ile Lys Met Gly Glu Ile Phe Val Asp Thr Pro Leu Thr Glu
    130                 135                 140
Ser Ile Lys Gln Leu Lys Leu Gln Thr Leu Glu Gly Phe Arg Gln Ile
145                 150                 155                 160
Leu Gln Ser Tyr Asn Thr Ala Leu Asp Asp Trp Arg Lys Leu Lys Arg
                165                 170                 175
Leu Gln Ala Pro Gly Leu Pro Pro Ser Ser Ala Leu Gln Gln Ala Ala
            180                 185                 190
Leu Thr Leu Lys Ile Arg Phe Glu Asn Val His Asn Asp Phe Ile Arg
        195                 200                 205
Glu Ile Pro Gly Phe Gln Leu Glu Thr Tyr Lys Thr Leu Leu Leu Pro
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    210                 215                 220
Ile Tyr Ala Gln Ala Ala Asn Phe His Leu Asn Leu Leu Gln Gln Gly
225                 230                 235                 240
Ala Glu Leu Ala Asp Glu Trp Asn Ala Asp Ile His Pro Ser Gln Ile
                245                 250                 255
Glu Pro Asn Ala Gly Thr Ser Asp Asp Tyr Tyr Lys Leu Leu Lys Glu
            260                 265                 270
Asn Ile Pro Lys Tyr Ser Asn Tyr Cys Ala Asn Thr Tyr Arg Thr Gly
        275                 280                 285
Leu Lys Asn Leu Arg Asp Glu Pro Asn Met Lys Trp Ser Ile Phe Asn
    290                 295                 300
Asp Tyr Arg Arg Tyr Met Thr Ile Thr Val Leu Asp Thr Ile Ser Gln
305                 310                 315                 320
Phe Ser Leu Tyr Asp Ile Lys Arg Tyr Arg Asp Ser Ile Gly Gly Ile
                325                 330                 335
Glu Val Lys Gly Ile Lys Asn Glu Leu Thr Arg Glu Ile Tyr Thr Thr
            340                 345                 350
Glu Ile Asn Phe Asp Arg Leu Pro Gln Leu Arg Val Gln Pro Asn Leu
        355                 360                 365
Ala Thr Met Glu Tyr Asn Leu Thr Arg Ala Ser Phe Lys Leu Phe Ser
    370                 375                 380
Phe Leu Glu Gln Phe Ile Phe Tyr Thr Glu Asn Thr Asn Phe Gly Asn
385                 390                 395                 400
Arg Leu Val Gly Ile Ser Asn Arg Asp Ala Pro Thr Tyr Ser Asn Thr
                405                 410                 415
Ile Thr Glu Thr Leu Tyr Gly Glu Arg Thr Gly Ser Pro Thr Thr Lys
            420                 425                 430
Thr Ile Arg Pro Phe Glu Ser Tyr Lys Val Ser Ile Val Thr Asp Arg
        435                 440                 445
Gln Ser Pro Pro Val Ser Pro Ile Gln Pro His Phe Ile Ile Asn Gln
    450                 455                 460
Ile Glu Leu Tyr Leu Asn Gly Ser Ser Asn Asn Thr Leu Lys Tyr Ser
465                 470                 475                 480
Ala Gly Gly Ser Leu Ser Asn Tyr Gln Asn Thr Thr Phe Phe Gln Phe
                485                 490                 495
Pro Arg Lys Lys Asp Cys Asn Leu Val Ile Asp Pro Gly Cys Ser Pro
            500                 505                 510
Asn Phe Asn Asn Tyr Ser His Ile Leu Ser His Phe Ser Leu Phe Thr
        515                 520                 525
Tyr Ser Tyr Val Ile Gly Leu Gln Leu Gln Ile Leu Asp Thr Gly Val
    530                 535                 540
Leu Gly Trp Thr His Ser Ser Val Asp Arg Tyr Asn Ala Ile Ser Asp
545                 550                 555                 560
Lys Ile Ile Thr Met Ile Pro Ala Ile Lys Gly Asn Asn Leu Asp Thr
                565                 570                 575
Asn Ser Lys Val Ile Glu Gly Pro Gly His Thr Gly Gly Asn Leu Val
            580                 585                 590
Tyr Leu Gln Ser Gln Gly Arg Leu Glu Ile Thr Cys Glu Thr Pro Asn
        595                 600                 605
Ser Thr Gln Ser Tyr Phe Ile Arg Leu Arg Tyr Ala Thr Asn Gly Ala
    610                 615                 620
Gly Asn Thr Leu Pro Asn Ile Ser Leu Thr Ile Pro Gly Val Ile Gly
625                 630                 635                 640
Ile Pro Pro Gln Arg Leu Asn Asn Thr Phe Ser Gly Thr Asn Tyr Asn
                645                 650                 655
Asn Leu Gln Tyr Gly Asp Phe Gly Tyr Phe Gln Phe Pro Ser Thr Val
            660                 665                 670
Thr Leu Pro Leu Asn Arg Asn Ile Pro Phe Ile Phe Asn Arg Ala Asp
        675                 680                 685
Val Ser Asn Ser Ile Leu Ile Ile Asp Lys Ile Glu Phe Ile Pro Ile
    690                 695                 700
Thr Ser Ser Met His Gln Asn Arg Glu Lys Gln Lys Leu Glu Thr Ile
705                 710                 715                 720
Gln Thr Lys Ile Asn Thr Phe Phe Thr Asn His Thr Lys Thr Leu
                725                 730                 735
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<210> 8

<211> 2235
<212> DNA
<213> Bacillus thuringiensis

<220>
<221> CDS
<222> (1)...(2235)

<400> 8

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gtg aat caa aat aat aat aat gaa tat gag att atc gat tca aag aat   48
Met Asn Gln Asn Asn Asn Asn Glu Tyr Glu Ile Ile Asp Ser Lys Asn
 1               5                  10                  15

tta tct tat cct tct aac aga aat att gat cat tct aga tac cct tac   96
Leu Ser Tyr Pro Ser Asn Arg Asn Ile Asp His Ser Arg Tyr Pro Tyr
            20                  25                  30

aca aat aat cca aat caa cca tta caa aac aca aat tac aaa gag tgg   144
Thr Asn Asn Pro Asn Gln Pro Leu Gln Asn Thr Asn Tyr Lys Glu Trp
        35                  40                  45

ctc aat atg tgt caa ggg aat aca caa tat ggt gat aat ttc gag aca   192
Leu Asn Met Cys Gln Gly Asn Thr Gln Tyr Gly Asp Asn Phe Glu Thr
    50                  55                  60

ttt gct agt gct gat aca att gct gca gtt agt gca ggt act att gta   240
Phe Ala Ser Ala Asp Thr Ile Ala Ala Val Ser Ala Gly Thr Ile Val
65                  70                  75                  80

tcc ggt act ctg tta gcc ggt ata ggt ggg ctc act tct ata tcc gga   288
Ser Gly Thr Leu Leu Ala Gly Ile Gly Gly Leu Thr Ser Ile Ser Gly
                85                  90                  95

ccg ata gga ata ata ggt gct ata ata ata tct ttt ggt acc cta atc   336
Pro Ile Gly Ile Ile Gly Ala Ile Ile Ile Ser Phe Gly Thr Leu Ile
            100                 105                 110

act gtc ttt tgg ccc gcg gga gaa caa gac aaa aca gta tgg aca caa   384
Thr Val Phe Trp Pro Ala Gly Glu Gln Asp Lys Thr Val Trp Thr Gln
        115                 120                 125

ttt att aaa atg gga gaa att ttt gtt gat aca ccg tta aca gaa agc   432
Phe Ile Lys Met Gly Glu Ile Phe Val Asp Thr Pro Leu Thr Glu Ser
    130                 135                 140

ata aaa cag cta aag tta caa act tta gaa gga ttt aga caa ata tta   480
Ile Lys Gln Leu Lys Leu Gln Thr Leu Glu Gly Phe Arg Gln Ile Leu
145                 150                 155                 160

caa agc tat aat aca gca tta gat gat tgg aga aaa tta aaa aga cta   528
Gln Ser Tyr Asn Thr Ala Leu Asp Asp Trp Arg Lys Leu Lys Arg Leu
                165                 170                 175

caa gct cct gga tta cca cca tca tca gca tta caa caa gct gcc ttg   576
Gln Ala Pro Gly Leu Pro Pro Ser Ser Ala Leu Gln Gln Ala Ala Leu
            180                 185                 190

act ctt aaa ata cga ttt gag aat gtt cac aat gat ttt att cga gaa   624
Thr Leu Lys Ile Arg Phe Glu Asn Val His Asn Asp Phe Ile Arg Glu
        195                 200                 205

ata cct ggt ttc caa ctt gaa act tat aaa acg cta tta cta cct att   672
Ile Pro Gly Phe Gln Leu Glu Thr Tyr Lys Thr Leu Leu Leu Pro Ile
    210                 215                 220

tat gcg caa gct gct aat ttt cat tta aat tta tta caa caa ggt gct   720
Tyr Ala Gln Ala Ala Asn Phe His Leu Asn Leu Leu Gln Gln Gly Ala
225                 230                 235                 240
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gaa ttg gct gat gaa tgg aat gca gat ata cat cct tca caa att gaa   768
Glu Leu Ala Asp Glu Trp Asn Ala Asp Ile His Pro Ser Gln Ile Glu
                245                 250                 255

cct aat gct gga aca tca gat gac tat tat aaa ctt tta aaa gaa aat   816
Pro Asn Ala Gly Thr Ser Asp Asp Tyr Tyr Lys Leu Leu Lys Glu Asn
            260                 265                 270

ata cct aaa tat agt aac tat tgt gca aat acc tat aga gaa gga cta   864
Ile Pro Lys Tyr Ser Asn Tyr Cys Ala Asn Thr Tyr Arg Glu Gly Leu
        275                 280                 285

aat aaa ctt cga aac gaa cct aat atg aga tgg agt ata ttt aat gat   912
Asn Lys Leu Arg Asn Glu Pro Asn Met Arg Trp Ser Ile Phe Asn Asp
    290                 295                 300

tat cga aga tat atg act att act gta tta gat act atc gct caa ttt   960
Tyr Arg Arg Tyr Met Thr Ile Thr Val Leu Asp Thr Ile Ala Gln Phe
305                 310                 315                 320

tct ttt tat gat ata aag aga tac aaa gat tca ata gga aga ata ggt   1008
Ser Phe Tyr Asp Ile Lys Arg Tyr Lys Asp Ser Ile Gly Arg Ile Gly
                325                 330                 335

ggc att aaa act gaa ctt aca aga gaa att tat aca act gaa ata aat   1056
Gly Ile Lys Thr Glu Leu Thr Arg Glu Ile Tyr Thr Thr Glu Ile Asn
            340                 345                 350

ttt gac cgt ctt act tac ctt gaa att caa ccc aat ctc gct ata atg   1104
Phe Asp Arg Leu Thr Tyr Leu Glu Ile Gln Pro Asn Leu Ala Ile Met
        355                 360                 365

gaa tat aat tta aca cgt tca ggg ctt aga tta ttt tca ttt tta gat   1152
Glu Tyr Asn Leu Thr Arg Ser Gly Leu Arg Leu Phe Ser Phe Leu Asp
    370                 375                 380

gaa ctt ata ttt tat aca aaa aat gaa acg tac ggg aat cgt tta gtt   1200
Glu Leu Ile Phe Tyr Thr Lys Asn Glu Thr Tyr Gly Asn Arg Leu Val
385                 390                 395                 400

ggt att gcg aat cgt aat aga tct act tat gct acg aca gga act gaa   1248
Gly Ile Ala Asn Arg Asn Arg Ser Thr Tyr Ala Thr Thr Gly Thr Glu
                405                 410                 415

att ata tat gga gaa aga aca ggt cca ccc aca aca aaa act tta ata   1296
Ile Ile Tyr Gly Glu Arg Thr Gly Pro Pro Thr Thr Lys Thr Leu Ile
            420                 425                 430

cca ttt gaa tcc tat aaa gtt tca att gta act gat aga caa gta act   1344
Pro Phe Glu Ser Tyr Lys Val Ser Ile Val Thr Asp Arg Gln Val Thr
        435                 440                 445

cct act tcc cct ttt cct aac ata tac ttt aca att aat caa att gaa   1392
Pro Thr Ser Pro Phe Pro Asn Ile Tyr Phe Thr Ile Asn Gln Ile Glu
    450                 455                 460

ctt tat tta aat aat tca cct agt aat aaa tta aca tat tca gct ggg   1440
Leu Tyr Leu Asn Asn Ser Pro Ser Asn Lys Leu Thr Tyr Ser Ala Gly
465                 470                 475                 480

ggg aat tta tct aat gat aaa aaa aca act gat ttt caa ttt cct gta   1488
Gly Asn Leu Ser Asn Asp Lys Lys Thr Thr Asp Phe Gln Phe Pro Val
                485                 490                 495

aaa aaa gac tgt aaa cca att att aat cca aat tgt tta cca agc tat   1536
Lys Lys Asp Cys Lys Pro Ile Ile Asn Pro Asn Cys Leu Pro Ser Tyr
            500                 505                 510
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aat agt tat agt cat att tta tcc cag ttt tct tta ttt aat tat tcc   1584
Asn Ser Tyr Ser His Ile Leu Ser Gln Phe Ser Leu Phe Asn Tyr Ser
        515                 520                 525

tat aaa att gga tta gcg cta aat ata tta tat aca ggt gca tta gga   1632
Tyr Lys Ile Gly Leu Ala Leu Asn Ile Leu Tyr Thr Gly Ala Leu Gly
    530                 535                 540

tgg aca cac agt agt gtt aat aga aat aat gca ata tca gat aaa ata   1680
Trp Thr His Ser Ser Val Asn Arg Asn Asn Ala Ile Ser Asp Lys Ile
545                 550                 555                 560

att aca atg atc cca gca atc aaa ggt aac agt ctt gat aca aac tct   1728
Ile Thr Met Ile Pro Ala Ile Lys Gly Asn Ser Leu Asp Thr Asn Ser
                565                 570                 575

aag gta att gaa gga cct ggt cat aca gga gga aac ttg gtt tat tta   1776
Lys Val Ile Glu Gly Pro Gly His Thr Gly Gly Asn Leu Val Tyr Leu
            580                 585                 590

caa agt caa ggg cgt tta gag att aca tgt aga act cct aat tct aca   1824
Gln Ser Gln Gly Arg Leu Glu Ile Thr Cys Arg Thr Pro Asn Ser Thr
        595                 600                 605

caa tct tat tac att aga ctt cga tac gct aca aat ggt gct gga aat   1872
Gln Ser Tyr Tyr Ile Arg Leu Arg Tyr Ala Thr Asn Gly Ala Gly Asn
    610                 615                 620

act ctt cct aat ata tct ctt aca ata cca gga gta ata gga ata cca   1920
Thr Leu Pro Asn Ile Ser Leu Thr Ile Pro Gly Val Ile Gly Ile Pro
625                 630                 635                 640

cct caa cga ctc aac aac act ttt tct ggt aca aat tat aat aat tta   1968
Pro Gln Arg Leu Asn Asn Thr Phe Ser Gly Thr Asn Tyr Asn Asn Leu
                645                 650                 655

caa tac gga gat ttt ggg tat ttc caa ttt cca agt aca gta aca tta   2016
Gln Tyr Gly Asp Phe Gly Tyr Phe Gln Phe Pro Ser Thr Val Thr Leu
            660                 665                 670

cct tta aat cga aac ata cca ttt ata ttt aat cgt gca gat gta tca   2064
Pro Leu Asn Arg Asn Ile Pro Phe Ile Phe Asn Arg Ala Asp Val Ser
        675                 680                 685

aat tca att tta atc att gat aaa att gaa ttt ata cca att act tcc   2112
Asn Ser Ile Leu Ile Ile Asp Lys Ile Glu Phe Ile Pro Ile Thr Ser
    690                 695                 700

tct gta cgc caa aat aga gaa aaa caa aaa tta gaa act atc caa aca   2160
Ser Val Arg Gln Asn Arg Glu Lys Gln Lys Leu Glu Thr Ile Gln Thr
705                 710                 715                 720

aaa ata aat aca ttt ttc aca aat cat aca aaa aat act tta aat ata   2208
Lys Ile Asn Thr Phe Phe Thr Asn His Thr Lys Asn Thr Leu Asn Ile
                725                 730                 735

gaa gcc aca aac tat gat att gat taa                             2235
Glu Ala Thr Asn Tyr Asp Ile Asp  *
            740
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<210> 9
<211> 744
<212> PRT
<213> Bacillus thuringiensis

<400> 9

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Met Asn Gln Asn Asn Asn Asn Glu Tyr Glu Ile Ile Asp Ser Lys Asn
 1               5                  10                  15
Leu Ser Tyr Pro Ser Asn Arg Asn Ile Asp His Ser Arg Tyr Pro Tyr
            20                  25                  30
Thr Asn Asn Pro Asn Gln Pro Leu Gln Asn Thr Asn Tyr Lys Glu Trp
        35                  40                  45
Leu Asn Met Cys Gln Gly Asn Thr Gln Tyr Gly Asp Asn Phe Glu Thr
    50                  55                  60
Phe Ala Ser Ala Asp Thr Ile Ala Ala Val Ser Ala Gly Thr Ile Val
65                  70                  75                  80
Ser Gly Thr Leu Leu Ala Gly Ile Gly Gly Leu Thr Ser Ile Ser Gly
                85                  90                  95
Pro Ile Gly Ile Ile Gly Ala Ile Ile Ile Ser Phe Gly Thr Leu Ile
            100                 105                 110
Thr Val Phe Trp Pro Ala Gly Glu Gln Asp Lys Thr Val Trp Thr Gln
        115                 120                 125
Phe Ile Lys Met Gly Glu Ile Phe Val Asp Thr Pro Leu Thr Glu Ser
    130                 135                 140
Tr  Lys Gln Leu Lys Leu Gln Thr Leu Glu Gly Phe Arg Gln Ile Leu
                150                 155                 160
 n Ser Tyr Asn Thr Ala Leu Asp Asp Trp Arg Lys Leu Lys Arg Leu
            165                 170                 175
Gln Ala Pro Gly Leu Pro Pro Ser Ser Ala Leu Gln Gln Ala Ala Leu
            180                 185                 190
Thr Leu Lys Ile Arg Phe Glu Asn Val His Asn Asp Phe Ile Arg Glu
        195                 200                 205
    Pro Gly Phe Gln Leu Glu Thr Tyr Lys Thr Leu Leu Leu Pro Ile
    210                 215                 220
Tyr Ala Gln Ala Ala Asn Phe His Leu Asn Leu Leu Gln Gln Gly Ala
225                 230                 235                 240
Glu Leu Ala Asp Glu Trp Asn Ala Asp Ile His Pro Ser Gln Ile Glu
                245                 250                 255
Pro Asn Ala Gly Thr Ser Asp Asp Tyr Tyr Lys Leu Leu Lys Glu Asn
            260                 265                 270
Ile Pro Lys Tyr Ser Asn Tyr Cys Ala Asn Thr Tyr Arg Glu Gly Leu
        275                 280                 285
Asn Lys Leu Arg Asn Glu Pro Asn Met Arg Trp Ser Ile Phe Asn Asp
    290                 295                 300
Tyr Arg Arg Tyr Met Thr Ile Thr Val Leu Asp Thr Ile Ala Gln Phe
305                 310                 315                 320
Ser Phe Tyr Asp Ile Lys Arg Tyr Lys Asp Ser Ile Gly Arg Ile Gly
                325                 330                 335
Gly Ile Lys Thr Glu Leu Thr Arg Glu Ile Tyr Thr Thr Glu Ile Asn
            340                 345                 350
Phe Asp Arg Leu Thr Tyr Leu Glu Ile Gln Pro Asn Leu Ala Ile Met
        355                 360                 365
Glu Tyr Asn Leu Thr Arg Ser Gly Leu Arg Leu Phe Ser Phe Leu Asp
    370                 375                 380
Glu Leu Ile Phe Tyr Thr Lys Asn Glu Thr Tyr Gly Asn Arg Leu Val
385                 390                 395                 400
Gly Ile Ala Asn Arg Asn Arg Ser Thr Tyr Ala Thr Thr Gly Thr Glu
                405                 410                 415
Ile Ile Tyr Gly Glu Arg Thr Gly Pro Pro Thr Thr Lys Thr Leu Ile
            420                 425                 430
Pro Phe Glu Ser Tyr Lys Val Ser Ile Val Thr Asp Arg Gln Val Thr
        435                 440                 445
Pro Thr Ser Pro Phe Pro Asn Ile Tyr Phe Thr Ile Asn Gln Ile Glu
    450                 455                 460
Leu Tyr Leu Asn Asn Ser Pro Ser Asn Lys Leu Thr Tyr Ser Ala Gly
465                 470                 475                 480
Gly Asn Leu Ser Asn Asp Lys Lys Thr Thr Asp Phe Gln Phe Pro Val
                485                 490                 495
Lys Lys Asp Cys Lys Pro Ile Ile Asn Pro Asn Cys Leu Pro Ser Tyr
            500                 505                 510
Asn Ser Tyr Ser His Ile Leu Ser Gln Phe Ser Leu Phe Asn Tyr Ser
        515                 520                 525
Tyr Lys Ile Gly Leu Ala Leu Asn Ile Leu Tyr Thr Gly Ala Leu Gly
    530                 535                 540
```

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Trp Thr His Ser Ser Val Asn Arg Asn Asn Ala Ile Ser Asp Lys Ile
545                 550                 555                 560
Ile Thr Met Ile Pro Ala Ile Lys Gly Asn Ser Leu Asp Thr Asn Ser
                565                 570                 575
Lys Val Ile Glu Gly Pro Gly His Thr Gly Gly Asn Leu Val Tyr Leu
            580                 585                 590
Gln Ser Gln Gly Arg Leu Glu Ile Thr Cys Arg Thr Pro Asn Ser Thr
        595                 600                 605
Gln Ser Tyr Tyr Ile Arg Leu Arg Tyr Ala Thr Asn Gly Ala Gly Asn
    610                 615                 620
Thr Leu Pro Asn Ile Ser Leu Thr Ile Pro Gly Val Ile Gly Ile Pro
625                 630                 635                 640
Pro Gln Arg Leu Asn Asn Thr Phe Ser Gly Thr Asn Tyr Asn Asn Leu
                645                 650                 655
Gln Tyr Gly Asp Phe Gly Tyr Phe Gln Phe Pro Ser Thr Val Thr Leu
            660                 665                 670
Pro Leu Asn Arg Asn Ile Pro Phe Ile Phe Asn Arg Ala Asp Val Ser
        675                 680                 685
Asn Ser Ile Leu Ile Ile Asp Lys Ile Glu Phe Ile Pro Ile Thr Ser
    690                 695                 700
Ser Val Arg Gln Asn Arg Glu Lys Gln Lys Leu Glu Thr Ile Gln Thr
705                 710                 715                 720
Lys Ile Asn Thr Phe Phe Thr Asn His Thr Lys Asn Thr Leu Asn Ile
                725                 730                 735
Glu Ala Thr Asn Tyr Asp Ile Asp
            740
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<210> 10
<211> 2085
<212> DNA
<213> Bacillus thuringiensis

<220>
<221> CDS
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<400> 10

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Met Cys Gln Gly Asn Thr Gln Tyr Gly Asp Asn Phe Glu Thr Phe Ala
 1               5                  10                  15

agt gct gat aca att gct gca gtt agt gca ggt act att gta tcc ggt   96
Ser Ala Asp Thr Ile Ala Ala Val Ser Ala Gly Thr Ile Val Ser Gly
            20                  25                  30

act ctg tta gcc ggt ata ggt ggg ctc act tct ata tcc gga ccg ata   144
Thr Leu Leu Ala Gly Ile Gly Gly Leu Thr Ser Ile Ser Gly Pro Ile
        35                  40                  45

gga ata ata ggt gct ata ata ata tct ttt ggt acc cta atc act gtc   192
Gly Ile Ile Gly Ala Ile Ile Ile Ser Phe Gly Thr Leu Ile Thr Val
    50                  55                  60

ttt tgg ccc gcg gga gaa caa gac aaa aca gta tgg aca caa ttt att   240
Phe Trp Pro Ala Gly Glu Gln Asp Lys Thr Val Trp Thr Gln Phe Ile
65                  70                  75                  80

aaa atg gga gaa att ttt gtt gat aca ccg tta aca gaa agc ata aaa   288
Lys Met Gly Glu Ile Phe Val Asp Thr Pro Leu Thr Glu Ser Ile Lys
                85                  90                  95

cag cta aag tta caa act tta gaa gga ttt aga caa ata tta caa agc   336
Gln Leu Lys Leu Gln Thr Leu Glu Gly Phe Arg Gln Ile Leu Gln Ser
            100                 105                 110

tat aat aca gca tta gat gat tgg aga aaa tta aaa aga cta caa gct   384
Tyr Asn Thr Ala Leu Asp Asp Trp Arg Lys Leu Lys Arg Leu Gln Ala
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        115                 120                 125

cct gga tta cca cca tca tca gca tta caa caa gct gcc ttg act ctt   432
Pro Gly Leu Pro Pro Ser Ser Ala Leu Gln Gln Ala Ala Leu Thr Leu
    130                 135                 140

aaa ata cga ttt gag aat gtt cac aat gat ttt att cga gaa ata cct   480
Lys Ile Arg Phe Glu Asn Val His Asn Asp Phe Ile Arg Glu Ile Pro
145                 150                 155                 160

ggt ttc caa ctt gaa act tat aaa acg cta tta cta cct att tat gcg   528
Gly Phe Gln Leu Glu Thr Tyr Lys Thr Leu Leu Leu Pro Ile Tyr Ala
                165                 170                 175

caa gct gct aat ttt cat tta aat tta tta caa caa ggt gct gaa ttg   576
Gln Ala Ala Asn Phe His Leu Asn Leu Leu Gln Gln Gly Ala Glu Leu
            180                 185                 190

gct gat gaa tgg aat gca gat ata cat cct tca caa att gaa cct aat   624
Ala Asp Glu Trp Asn Ala Asp Ile His Pro Ser Gln Ile Glu Pro Asn
        195                 200                 205

gct gga aca tca gat gac tat tat aaa ctt tta aaa gaa aat ata cct   672
Ala Gly Thr Ser Asp Asp Tyr Tyr Lys Leu Leu Lys Glu Asn Ile Pro
    210                 215                 220

aaa tat agt aac tat tgt gca aat acc tat aga gaa gga cta aat aaa   720
Lys Tyr Ser Asn Tyr Cys Ala Asn Thr Tyr Arg Glu Gly Leu Asn Lys
225                 230                 235                 240

ctt cga aac gaa cct aat atg aga tgg agt ata ttt aat gat tat cga   768
Leu Arg Asn Glu Pro Asn Met Arg Trp Ser Ile Phe Asn Asp Tyr Arg
                245                 250                 255

aga tat atg act att act gta tta gat act atc gct caa ttt tct ttt   816
Arg Tyr Met Thr Ile Thr Val Leu Asp Thr Ile Ala Gln Phe Ser Phe
            260                 265                 270

tat gat ata aag aga tac aaa gat tca ata gga aga ata ggt ggc att   864
Tyr Asp Ile Lys Arg Tyr Lys Asp Ser Ile Gly Arg Ile Gly Gly Ile
        275                 280                 285

aaa act gaa ctt aca aga gaa att tat aca act gaa ata aat ttt gac   912
Lys Thr Glu Leu Thr Arg Glu Ile Tyr Thr Thr Glu Ile Asn Phe Asp
    290                 295                 300

cgt ctt act tac ctt gaa att caa ccc aat ctc gct ata atg gaa tat   960
Arg Leu Thr Tyr Leu Glu Ile Gln Pro Asn Leu Ala Ile Met Glu Tyr
305                 310                 315                 320

aat tta aca cgt tca ggg ctt aga tta ttt tca ttt tta gat gaa ctt   1008
Asn Leu Thr Arg Ser Gly Leu Arg Leu Phe Ser Phe Leu Asp Glu Leu
                325                 330                 335

ata ttt tat aca aaa aat gaa acg tac ggg aat cgt tta gtt ggt att   1056
Ile Phe Tyr Thr Lys Asn Glu Thr Tyr Gly Asn Arg Leu Val Gly Ile
            340                 345                 350

gcg aat cgt aat aga tct act tat gct acg aca gga act gaa att ata   1104
Ala Asn Arg Asn Arg Ser Thr Tyr Ala Thr Thr Gly Thr Glu Ile Ile
        355                 360                 365

tat gga gaa aga aca ggt cca ccc aca aca aaa act tta ata cca ttt   1152
Tyr Gly Glu Arg Thr Gly Pro Pro Thr Thr Lys Thr Leu Ile Pro Phe
    370                 375                 380

gaa tcc tat aaa gtt tca att gta act gat aga caa gta act cct act   1200
Glu Ser Tyr Lys Val Ser Ile Val Thr Asp Arg Gln Val Thr Pro Thr
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385                 390                 395                 400

tcc cct ttt cct aac ata tac ttt aca att aat caa att gaa ctt tat   1248
Ser Pro Phe Pro Asn Ile Tyr Phe Thr Ile Asn Gln Ile Glu Leu Tyr
                405                 410                 415

tta aat aat tca cct agt aat aaa tta aca tat tca gct ggg ggg aat   1296
Leu Asn Asn Ser Pro Ser Asn Lys Leu Thr Tyr Ser Ala Gly Gly Asn
            420                 425                 430

tta tct aat gat aaa aaa aca act gat ttt caa ttt cct gta aaa aaa   1344
Leu Ser Asn Asp Lys Lys Thr Thr Asp Phe Gln Phe Pro Val Lys Lys
        435                 440                 445

gac tgt aaa cca att att aat cca aat tgt tta cca agc tat aat agt   1392
Asp Cys Lys Pro Ile Ile Asn Pro Asn Cys Leu Pro Ser Tyr Asn Ser
    450                 455                 460

tat agt cat att tta tcc cag ttt tct tta ttt aat tat tcc tat aaa   1440
Tyr Ser His Ile Leu Ser Gln Phe Ser Leu Phe Asn Tyr Ser Tyr Lys
465                 470                 475                 480

att gga tta gcg cta aat ata tta tat aca ggt gca tta gga tgg aca   1488
Ile Gly Leu Ala Leu Asn Ile Leu Tyr Thr Gly Ala Leu Gly Trp Thr
                485                 490                 495

cac agt agt gtt aat aga aat aat gca ata tca gat aaa ata att aca   1536
His Ser Ser Val Asn Arg Asn Asn Ala Ile Ser Asp Lys Ile Ile Thr
            500                 505                 510

atg atc cca gca atc aaa ggt aac agt ctt gat aca aac tct aag gta   1584
Met Ile Pro Ala Ile Lys Gly Asn Ser Leu Asp Thr Asn Ser Lys Val
        515                 520                 525

att gaa gga cct ggt cat aca gga gga aac ttg gtt tat tta caa agt   1632
Ile Glu Gly Pro Gly His Thr Gly Gly Asn Leu Val Tyr Leu Gln Ser
    530                 535                 540

caa ggg cgt tta gag att aca tgt aga act cct aat tct aca caa tct   1680
Gln Gly Arg Leu Glu Ile Thr Cys Arg Thr Pro Asn Ser Thr Gln Ser
545                 550                 555                 560

tat tac att aga ctt cga tac gct aca aat ggt gct gga aat act ctt   1728
Tyr Tyr Ile Arg Leu Arg Tyr Ala Thr Asn Gly Ala Gly Asn Thr Leu
                565                 570                 575

cct aat ata tct ctt aca ata cca gga gta ata gga ata cca cct caa   1776
Pro Asn Ile Ser Leu Thr Ile Pro Gly Val Ile Gly Ile Pro Pro Gln
            580                 585                 590

cga ctc aac aac act ttt tct ggt aca aat tat aat aat tta caa tac   1824
Arg Leu Asn Asn Thr Phe Ser Gly Thr Asn Tyr Asn Asn Leu Gln Tyr
        595                 600                 605

gga gat ttt ggg tat ttc caa ttt cca agt aca gta aca tta cct tta   1872
Gly Asp Phe Gly Tyr Phe Gln Phe Pro Ser Thr Val Thr Leu Pro Leu
    610                 615                 620

aat cga aac ata cca ttt ata ttt aat cgt gca gat gta tca aat tca   1920
Asn Arg Asn Ile Pro Phe Ile Phe Asn Arg Ala Asp Val Ser Asn Ser
625                 630                 635                 640

att tta atc att gat aaa att gaa ttt ata cca att act tcc tct gta   1968
Ile Leu Ile Ile Asp Lys Ile Glu Phe Ile Pro Ile Thr Ser Ser Val
                645                 650                 655

cgc caa aat aga gaa aaa caa aaa tta gaa act atc caa aca aaa ata   2016
Arg Gln Asn Arg Glu Lys Gln Lys Leu Glu Thr Ile Gln Thr Lys Ile
```

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            660                 665                 670

aat aca ttt ttc aca aat cat aca aaa aat act tta aat ata gaa gcc   2064
Asn Thr Phe Phe Thr Asn His Thr Lys Asn Thr Leu Asn Ile Glu Ala
        675                 680                 685

aca aac tat gat att gat taa                                      2085
Thr Asn Tyr Asp Ile Asp  *
    690
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<210> 11
<211> 694
<212> PRT
<213> Bacillus thuringiensis

<400> 11

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Met Cys Gln Gly Asn Thr Gln Tyr Gly Asp Asn Phe Glu Thr Phe Ala
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Ser Ala Asp Thr Ile Ala Ala Val Ser Ala Gly Thr Ile Val Ser Gly
            20                  25                  30
Thr Leu Leu Ala Gly Ile Gly Gly Leu Thr Ser Ile Ser Gly Pro Ile
        35                  40                  45
Gly Ile Ile Gly Ala Ile Ile Ile Ser Phe Gly Thr Leu Ile Thr Val
    50                  55                  60
Phe Trp Pro Ala Gly Glu Gln Asp Lys Thr Val Trp Thr Gln Phe Ile
65                  70                  75                  80
Lys Met Gly Glu Ile Phe Val Asp Thr Pro Leu Thr Glu Ser Ile Lys
                85                  90                  95
Gln Leu Lys Leu Gln Thr Leu Glu Gly Phe Arg Gln Ile Leu Gln Ser
            100                 105                 110
Tyr Asn Thr Ala Leu Asp Asp Trp Arg Lys Leu Lys Arg Leu Gln Ala
        115                 120                 125
Pro Gly Leu Pro Pro Ser Ser Ala Leu Gln Gln Ala Ala Leu Thr Leu
    130                 135                 140
Lys Ile Arg Phe Glu Asn Val His Asn Asp Phe Ile Arg Glu Ile Pro
145                 150                 155                 160
Gly Phe Gln Leu Glu Thr Tyr Lys Thr Leu Leu Leu Pro Ile Tyr Ala
                165                 170                 175
Gln Ala Ala Asn Phe His Leu Asn Leu Leu Gln Gln Gly Ala Glu Leu
            180                 185                 190
Ala Asp Glu Trp Asn Ala Asp Ile His Pro Ser Gln Ile Glu Pro Asn
        195                 200                 205
Ala Gly Thr Ser Asp Asp Tyr Tyr Lys Leu Leu Lys Glu Asn Ile Pro
    210                 215                 220
Lys Tyr Ser Asn Tyr Cys Ala Asn Thr Tyr Arg Glu Gly Leu Asn Lys
225                 230                 235                 240
Leu Arg Asn Glu Pro Asn Met Arg Trp Ser Ile Phe Asn Asp Tyr Arg
                245                 250                 255
Arg Tyr Met Thr Ile Thr Val Leu Asp Thr Ile Ala Gln Phe Ser Phe
            260                 265                 270
Tyr Asp Ile Lys Arg Tyr Lys Asp Ser Ile Gly Arg Ile Gly Gly Ile
        275                 280                 285
Lys Thr Glu Leu Thr Arg Glu Ile Tyr Thr Thr Glu Ile Asn Phe Asp
    290                 295                 300
Arg Leu Thr Tyr Leu Glu Ile Gln Pro Asn Leu Ala Ile Met Glu Tyr
305                 310                 315                 320
Asn Leu Thr Arg Ser Gly Leu Arg Leu Phe Ser Phe Leu Asp Glu Leu
                325                 330                 335
Ile Phe Tyr Thr Lys Asn Glu Thr Tyr Gly Asn Arg Leu Val Gly Ile
            340                 345                 350
Ala Asn Arg Asn Arg Ser Thr Tyr Ala Thr Thr Gly Thr Glu Ile Ile
        355                 360                 365
Tyr Gly Glu Arg Thr Gly Pro Pro Thr Thr Lys Thr Leu Ile Pro Phe
    370                 375                 380
Glu Ser Tyr Lys Val Ser Ile Val Thr Asp Arg Gln Val Thr Pro Thr
385                 390                 395                 400
Ser Pro Phe Pro Asn Ile Tyr Phe Thr Ile Asn Gln Ile Glu Leu Tyr
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                405                 410                 415
Leu Asn Asn Ser Pro Ser Asn Lys Leu Thr Tyr Ser Ala Gly Gly Asn
            420                 425                 430
Leu Ser Asn Asp Lys Lys Thr Thr Asp Phe Gln Phe Pro Val Lys Lys
        435                 440                 445
Asp Cys Lys Pro Ile Ile Asn Pro Asn Cys Leu Pro Ser Tyr Asn Ser
    450                 455                 460
Tyr Ser His Ile Leu Ser Gln Phe Ser Leu Phe Asn Tyr Ser Tyr Lys
465                 470                 475                 480
Ile Gly Leu Ala Leu Asn Ile Leu Tyr Thr Gly Ala Leu Gly Trp Thr
                485                 490                 495
His Ser Ser Val Asn Arg Asn Asn Ala Ile Ser Asp Lys Ile Ile Thr
            500                 505                 510
Met Ile Pro Ala Ile Lys Gly Asn Ser Leu Asp Thr Asn Ser Lys Val
        515                 520                 525
Ile Glu Gly Pro Gly His Thr Gly Gly Asn Leu Val Tyr Leu Gln Ser
    530                 535                 540
Gln Gly Arg Leu Glu Ile Thr Cys Arg Thr Pro Asn Ser Thr Gln Ser
545                 550                 555                 560
Tyr Tyr Ile Arg Leu Arg Tyr Ala Thr Asn Gly Ala Gly Asn Thr Leu
                565                 570                 575
Pro Asn Ile Ser Leu Thr Ile Pro Gly Val Ile Gly Ile Pro Pro Gln
            580                 585                 590
Arg Leu Asn Asn Thr Phe Ser Gly Thr Asn Tyr Asn Asn Leu Gln Tyr
        595                 600                 605
Gly Asp Phe Gly Tyr Phe Gln Phe Pro Ser Thr Val Thr Leu Pro Leu
    610                 615                 620
Asn Arg Asn Ile Pro Phe Ile Phe Asn Arg Ala Asp Val Ser Asn Ser
625                 630                 635                 640
Ile Leu Ile Ile Asp Lys Ile Glu Phe Ile Pro Ile Thr Ser Ser Val
                645                 650                 655
Arg Gln Asn Arg Glu Lys Gln Lys Leu Glu Thr Ile Gln Thr Lys Ile
            660                 665                 670
Asn Thr Phe Phe Thr Asn His Thr Lys Asn Thr Leu Asn Ile Glu Ala
        675                 680                 685
Thr Asn Tyr Asp Ile Asp
    690
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<210> 12
<211> 5980
<212> DNA
<213> Bacillus thruingiensis

<400> 12

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ttaaactttc agaaagagat ttcaatgaaa ttctaggagg gtcattgtca agaaacaatg 720
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gtaacggtat ttttcaacgt atgtctggaa ctacgagtaa tgatctacgt aatattgatt 1380
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<210> 13
<211> 2082
<212> DNA
<213> Bacillus thuringiensis

<220>
<221> CDS
<222> (1)...(2082)

<400> 13

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gtg aaa aag atg agt cca tat caa aat aaa aat gaa tat gaa ata ttg   48
Met Lys Lys Met Ser Pro Tyr Gln Asn Lys Asn Glu Tyr Glu Ile Leu
 1               5                  10                  15

gaa tcc tca tcg aat aac aca aat acg cca aac aga tat cct ttt gca   96
Glu Ser Ser Ser Asn Asn Thr Asn Thr Pro Asn Arg Tyr Pro Phe Ala
            20                  25                  30

aat aat cgg gat atg tct act atg tct tgg aat gat tgt cag gga atc   144
Asn Asn Arg Asp Met Ser Thr Met Ser Trp Asn Asp Cys Gln Gly Ile
        35                  40                  45

tca tgg gat gaa att tgg gaa tca gtc gaa acg ata aca agt att ggg   192
Ser Trp Asp Glu Ile Trp Glu Ser Val Glu Thr Ile Thr Ser Ile Gly
    50                  55                  60

ata aat ctt ata gag ttt gtg ata gaa cct agt ttg ggt gga att aat   240
Ile Asn Leu Ile Glu Phe Val Ile Glu Pro Ser Leu Gly Gly Ile Asn
65                  70                  75                  80

aca cta tta tca ata ata gga aaa cta att ccg act aat cgt caa act   288
Thr Leu Leu Ser Ile Ile Gly Lys Leu Ile Pro Thr Asn Arg Gln Thr
                85                  90                  95

gtg tca gca ctt tct ata tgt gat tta tta tct ata att cgt aaa gag   336
Val Ser Ala Leu Ser Ile Cys Asp Leu Leu Ser Ile Ile Arg Lys Glu
            100                 105                 110

gta gcc gat agt gtt tta agt gat gcg att gca gat ttt gac ggt aaa   384
Val Ala Asp Ser Val Leu Ser Asp Ala Ile Ala Asp Phe Asp Gly Lys
        115                 120                 125

ttg aaa aat tat aga gag tat tat ctt tct tat ctt ggg gct tgg ctt   432
Leu Lys Asn Tyr Arg Glu Tyr Tyr Leu Ser Tyr Leu Gly Ala Trp Leu
    130                 135                 140

aaa gac ggt aaa cca ctt caa aag aca aat aat tct gat atc gga caa   480
Lys Asp Gly Lys Pro Leu Gln Lys Thr Asn Asn Ser Asp Ile Gly Gln
145                 150                 155                 160

tta gtt tat tat ttt aaa ctt tca gaa aga gat ttc aat gaa att cta   528
Leu Val Tyr Tyr Phe Lys Leu Ser Glu Arg Asp Phe Asn Glu Ile Leu
                165                 170                 175

gga ggg tca ttg tca aga aac aat gct caa gta ttg tta tta cct act   576
Gly Gly Ser Leu Ser Arg Asn Asn Ala Gln Val Leu Leu Leu Pro Thr
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            180                 185                 190

ttt gca caa gct gca aat gtg cag tta tta cta tta agg gat gca gtt   624
Phe Ala Gln Ala Ala Asn Val Gln Leu Leu Leu Leu Arg Asp Ala Val
        195                 200                 205

caa tat aaa gca caa tgg ttc cca ttt ttg agt gca gag aat gta aga   672
Gln Tyr Lys Ala Gln Trp Phe Pro Phe Leu Ser Ala Glu Asn Val Arg
    210                 215                 220

tcg gaa tta ata tca cct aac agt ggt tgt gat ttt acc ggt gat tac   720
Ser Glu Leu Ile Ser Pro Asn Ser Gly Cys Asp Phe Thr Gly Asp Tyr
225                 230                 235                 240

tat gag cga tta aaa tgc aaa acg gca gag tat acc aat tat tgt tta   768
Tyr Glu Arg Leu Lys Cys Lys Thr Ala Glu Tyr Thr Asn Tyr Cys Leu
                245                 250                 255

tat tgg tat cag gta ggt tta aat cag ata aaa cag ggg ggg aca ggt   816
Tyr Trp Tyr Gln Val Gly Leu Asn Gln Ile Lys Gln Gly Gly Thr Gly
            260                 265                 270

gct gac act tgg tcg aaa ttt aat aaa ttt cgt aga gaa atg acg ttg   864
Ala Asp Thr Trp Ser Lys Phe Asn Lys Phe Arg Arg Glu Met Thr Leu
        275                 280                 285

gcg gta ttg gat att atc gct ata ttt cca act tat gat ttt gag aaa   912
Ala Val Leu Asp Ile Ile Ala Ile Phe Pro Thr Tyr Asp Phe Glu Lys
    290                 295                 300

tat cca ttg cca aca cat gta gag ttg act agg gaa att tat aca gat   960
Tyr Pro Leu Pro Thr His Val Glu Leu Thr Arg Glu Ile Tyr Thr Asp
305                 310                 315                 320

gca gtg gga tat tca tcg gga act tat agt tgg tta cgg aat tgg cct  1008
Ala Val Gly Tyr Ser Ser Gly Thr Tyr Ser Trp Leu Arg Asn Trp Pro
                325                 330                 335

aat act ttt aat ggg tta gag gct aat gga aca cgg gga cct ggt tta  1056
Asn Thr Phe Asn Gly Leu Glu Ala Asn Gly Thr Arg Gly Pro Gly Leu
            340                 345                 350

gtt act tgg ctt agc aaa ata ggt ata tat aat gag tat gtt tcg aga  1104
Val Thr Trp Leu Ser Lys Ile Gly Ile Tyr Asn Glu Tyr Val Ser Arg
        355                 360                 365

tat ttt gcc ggc tgg gta gga act cgt cat tat gaa gac tac aca aag  1152
Tyr Phe Ala Gly Trp Val Gly Thr Arg His Tyr Glu Asp Tyr Thr Lys
    370                 375                 380

ggt aac ggt att ttt caa cgt atg tct gga act acg agt aat gat cta  1200
Gly Asn Gly Ile Phe Gln Arg Met Ser Gly Thr Thr Ser Asn Asp Leu
385                 390                 395                 400

cgt aat att gat ttt cag aat gcc gat gta tat aaa att act tca tta  1248
Arg Asn Ile Asp Phe Gln Asn Ala Asp Val Tyr Lys Ile Thr Ser Leu
                405                 410                 415

gct atc atg aac cta gta gga gag act acc gct aga cca gag tat cgt  1296
Ala Ile Met Asn Leu Val Gly Glu Thr Thr Ala Arg Pro Glu Tyr Arg
            420                 425                 430

gtt tca aag gca gat ttt cgt agg gta ggg gga cct gat tta aat tat  1344
Val Ser Lys Ala Asp Phe Arg Arg Val Gly Gly Pro Asp Leu Asn Tyr
        435                 440                 445

gat gca ggt aat aat ggg cta agc agg atg aca att gaa tct acg ttc  1392
Asp Ala Gly Asn Asn Gly Leu Ser Arg Met Thr Ile Glu Ser Thr Phe
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    450                 455                 460

cca ctt gta ttg cac tct aat ggt gtt aga gga ccc tct cat aga tta   1440
Pro Leu Val Leu His Ser Asn Gly Val Arg Gly Pro Ser His Arg Leu
465                 470                 475                 480

tca aat gcg gca tgt gtt gta tat gga aac tcc aga gtt aac gta tat   1488
Ser Asn Ala Ala Cys Val Val Tyr Gly Asn Ser Arg Val Asn Val Tyr
                485                 490                 495

ggt tgg aca cat aca agt tta aaa cgt gaa aat ata att gaa gcc aat   1536
Gly Trp Thr His Thr Ser Leu Lys Arg Glu Asn Ile Ile Glu Ala Asn
            500                 505                 510

caa att aca caa ata ccg gcg gtg aag agt tat tac ctt caa aat tat   1584
Gln Ile Thr Gln Ile Pro Ala Val Lys Ser Tyr Tyr Leu Gln Asn Tyr
        515                 520                 525

ctt gct aat gcc tat acc tat gta ata aaa ggc act cat aca ggt ggg   1632
Leu Ala Asn Ala Tyr Thr Tyr Val Ile Lys Gly Thr His Thr Gly Gly
    530                 535                 540

gat tta atc cgt ttt tta aga aca aaa tca gag tat aac gca gtt tat   1680
Asp Leu Ile Arg Phe Leu Arg Thr Lys Ser Glu Tyr Asn Ala Val Tyr
545                 550                 555                 560

gca ggt ggc gga att aga ttg att att aat aac aaa act gca gga caa   1728
Ala Gly Gly Gly Ile Arg Leu Ile Ile Asn Asn Lys Thr Ala Gly Gln
                565                 570                 575

agt tac cgt att cgt ttt cgt tat gct gca gat aaa gct gct ttc ttt   1776
Ser Tyr Arg Ile Arg Phe Arg Tyr Ala Ala Asp Lys Ala Ala Phe Phe
            580                 585                 590

agt gta tat ctt tat cca gga ggt tgg ggt tca aat cgt ttt gta tcg   1824
Ser Val Tyr Leu Tyr Pro Gly Gly Trp Gly Ser Asn Arg Phe Val Ser
        595                 600                 605

ctt gaa aaa tct tac tct gga aat tat gac gat tta aaa tat agt gat   1872
Leu Glu Lys Ser Tyr Ser Gly Asn Tyr Asp Asp Leu Lys Tyr Ser Asp
    610                 615                 620

ttt aaa ttc gct gaa att atc aca cct cca tta cct agt tca aac att   1920
Phe Lys Phe Ala Glu Ile Ile Thr Pro Pro Leu Pro Ser Ser Asn Ile
625                 630                 635                 640

cag atg gat gtg gag atg caa gcg aat agt ttt caa tca gat gta aac   1968
Gln Met Asp Val Glu Met Gln Ala Asn Ser Phe Gln Ser Asp Val Asn
                645                 650                 655

gtg gtt ctc gac aaa att gaa ttc ctc cca agt aat aca aca act tta   2016
Val Val Leu Asp Lys Ile Glu Phe Leu Pro Ser Asn Thr Thr Thr Leu
            660                 665                 670

gaa tat gag gga gaa cgg gac cta gaa aaa aca aag aac gcg gtg aac   2064
Glu Tyr Glu Gly Glu Arg Asp Leu Glu Lys Thr Lys Asn Ala Val Asn
        675                 680                 685

gat ctg ttt acc aat taa                                          2082
Asp Leu Phe Thr Asn  *
    690
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<210> 14
<211> 693
<212> PRT
<213> Bacillus thuringiensis

<400> 14

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Met Lys Lys Met Ser Pro Tyr Gln Asn Lys Asn Glu Tyr Glu Ile Leu
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Glu Ser Ser Ser Asn Asn Thr Asn Thr Pro Asn Arg Tyr Pro Phe Ala
            20                  25                  30
Asn Asn Arg Asp Met Ser Thr Met Ser Trp Asn Asp Cys Gln Gly Ile
        35                  40                  45
Ser Trp Asp Glu Ile Trp Glu Ser Val Glu Thr Ile Thr Ser Ile Gly
    50                  55                  60
Ile Asn Leu Ile Glu Phe Val Ile Glu Pro Ser Leu Gly Gly Ile Asn
65                  70                  75                  80
Thr Leu Leu Ser Ile Ile Gly Lys Leu Ile Pro Thr Asn Arg Gln Thr
                85                  90                  95
Val Ser Ala Leu Ser Ile Cys Asp Leu Leu Ser Ile Ile Arg Lys Glu
            100                 105                 110
Val Ala Asp Ser Val Leu Ser Asp Ala Ile Ala Asp Phe Asp Gly Lys
        115                 120                 125
Leu Lys Asn Tyr Arg Glu Tyr Tyr Leu Ser Tyr Leu Gly Ala Trp Leu
    130                 135                 140
Lys Asp Gly Lys Pro Leu Gln Lys Thr Asn Asn Ser Asp Ile Gly Gln
145                 150                 155                 160
Leu Val Tyr Tyr Phe Lys Leu Ser Glu Arg Asp Phe Asn Glu Ile Leu
                165                 170                 175
Gly Gly Ser Leu Ser Arg Asn Asn Ala Gln Val Leu Leu Leu Pro Thr
            180                 185                 190
Phe Ala Gln Ala Ala Asn Val Gln Leu Leu Leu Leu Arg Asp Ala Val
        195                 200                 205
Gln Tyr Lys Ala Gln Trp Phe Pro Phe Leu Ser Ala Glu Asn Val Arg
    210                 215                 220
Ser Glu Leu Ile Ser Pro Asn Ser Gly Cys Asp Phe Thr Gly Asp Tyr
225                 230                 235                 240
Tyr Glu Arg Leu Lys Cys Lys Thr Ala Glu Tyr Thr Asn Tyr Cys Leu
                245                 250                 255
Tyr Trp Tyr Gln Val Gly Leu Asn Gln Ile Lys Gln Gly Gly Thr Gly
            260                 265                 270
Ala Asp Thr Trp Ser Lys Phe Asn Lys Phe Arg Arg Glu Met Thr Leu
        275                 280                 285
Ala Val Leu Asp Ile Ile Ala Ile Phe Pro Thr Tyr Asp Phe Glu Lys
    290                 295                 300
Tyr Pro Leu Pro Thr His Val Glu Leu Thr Arg Glu Ile Tyr Thr Asp
305                 310                 315                 320
Ala Val Gly Tyr Ser Ser Gly Thr Tyr Ser Trp Leu Arg Asn Trp Pro
                325                 330                 335
Asn Thr Phe Asn Gly Leu Glu Ala Asn Gly Thr Arg Gly Pro Gly Leu
            340                 345                 350
Val Thr Trp Leu Ser Lys Ile Gly Ile Tyr Asn Glu Tyr Val Ser Arg
        355                 360                 365
Tyr Phe Ala Gly Trp Val Gly Thr Arg His Tyr Glu Asp Tyr Thr Lys
    370                 375                 380
Gly Asn Gly Ile Phe Gln Arg Met Ser Gly Thr Thr Ser Asn Asp Leu
385                 390                 395                 400
Arg Asn Ile Asp Phe Gln Asn Ala Asp Val Tyr Lys Ile Thr Ser Leu
                405                 410                 415
Ala Ile Met Asn Leu Val Gly Glu Thr Thr Ala Arg Pro Glu Tyr Arg
            420                 425                 430
Val Ser Lys Ala Asp Phe Arg Arg Val Gly Gly Pro Asp Leu Asn Tyr
        435                 440                 445
Asp Ala Gly Asn Asn Gly Leu Ser Arg Met Thr Ile Glu Ser Thr Phe
    450                 455                 460
Pro Leu Val Leu His Ser Asn Gly Val Arg Gly Pro Ser His Arg Leu
465                 470                 475                 480
Ser Asn Ala Ala Cys Val Val Tyr Gly Asn Ser Arg Val Asn Val Tyr
                485                 490                 495
Gly Trp Thr His Thr Ser Leu Lys Arg Glu Asn Ile Ile Glu Ala Asn
            500                 505                 510
Gln Ile Thr Gln Ile Pro Ala Val Lys Ser Tyr Tyr Leu Gln Asn Tyr
        515                 520                 525
Leu Ala Asn Ala Tyr Thr Tyr Val Ile Lys Gly Thr His Thr Gly Gly
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    530                 535                 540
Asp Leu Ile Arg Phe Leu Arg Thr Lys Ser Glu Tyr Asn Ala Val Tyr
545                 550                 555                 560
Ala Gly Gly Gly Ile Arg Leu Ile Ile Asn Asn Lys Thr Ala Gly Gln
                565                 570                 575
Ser Tyr Arg Ile Arg Phe Arg Tyr Ala Ala Asp Lys Ala Ala Phe Phe
            580                 585                 590
Ser Val Tyr Leu Tyr Pro Gly Gly Trp Gly Ser Asn Arg Phe Val Ser
        595                 600                 605
Leu Glu Lys Ser Tyr Ser Gly Asn Tyr Asp Asp Leu Lys Tyr Ser Asp
    610                 615                 620
Phe Lys Phe Ala Glu Ile Ile Thr Pro Pro Leu Pro Ser Ser Asn Ile
625                 630                 635                 640
Gln Met Asp Val Glu Met Gln Ala Asn Ser Phe Gln Ser Asp Val Asn
                645                 650                 655
Val Val Leu Asp Lys Ile Glu Phe Leu Pro Ser Asn Thr Thr Thr Leu
            660                 665                 670
Glu Tyr Glu Gly Glu Arg Asp Leu Glu Lys Thr Lys Asn Ala Val Asn
        675                 680                 685
Asp Leu Phe Thr Asn
    690
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<210> 15
<211> 2073
<212> DNA
<213> Bacillus thuringiensis

<220>
<221> CDS
<222> (1)...(2073)

<400> 15

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atg agt cca tat caa aat aaa aat gaa tat gaa ata ttg gaa tcc tca   48
Met Ser Pro Tyr Gln Asn Lys Asn Glu Tyr Glu Ile Leu Glu Ser Ser
 1               5                  10                  15

tcg aat aac aca aat acg cca aac aga tat cct ttt gca aat aat cgg   96
Ser Asn Asn Thr Asn Thr Pro Asn Arg Tyr Pro Phe Ala Asn Asn Arg
            20                  25                  30

gat atg tct act atg tct tgg aat gat tgt cag gga atc tca tgg gat   144
Asp Met Ser Thr Met Ser Trp Asn Asp Cys Gln Gly Ile Ser Trp Asp
        35                  40                  45

gaa att tgg gaa tca gtc gaa acg ata aca agt att ggg ata aat ctt   192
Glu Ile Trp Glu Ser Val Glu Thr Ile Thr Ser Ile Gly Ile Asn Leu
    50                  55                  60

ata gag ttt gtg ata gaa cct agt ttg ggt gga att aat aca cta tta   240
Ile Glu Phe Val Ile Glu Pro Ser Leu Gly Gly Ile Asn Thr Leu Leu
65                  70                  75                  80

tca ata ata gga aaa cta att ccg act aat cgt caa act gtg tca gca   288
Ser Ile Ile Gly Lys Leu Ile Pro Thr Asn Arg Gln Thr Val Ser Ala
                85                  90                  95

ctt tct ata tgt gat tta tta tct ata att cgt aaa gag gta gcc gat   336
Leu Ser Ile Cys Asp Leu Leu Ser Ile Ile Arg Lys Glu Val Ala Asp
            100                 105                 110

agt gtt tta agt gat gcg att gca gat ttt gac ggt aaa ttg aaa aat   384
Ser Val Leu Ser Asp Ala Ile Ala Asp Phe Asp Gly Lys Leu Lys Asn
        115                 120                 125

tat aga gag tat tat ctt tct tat ctt ggg gct tgg ctt aaa gac ggt   432
Tyr Arg Glu Tyr Tyr Leu Ser Tyr Leu Gly Ala Trp Leu Lys Asp Gly
    130                 135                 140
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aaa cca ctt caa aag aca aat aat tct gat atc gga caa tta gtt tat   480
Lys Pro Leu Gln Lys Thr Asn Asn Ser Asp Ile Gly Gln Leu Val Tyr
145                 150                 155                 160

tat ttt aaa ctt tca gaa aga gat ttc aat gaa att cta gga ggg tca   528
Tyr Phe Lys Leu Ser Glu Arg Asp Phe Asn Glu Ile Leu Gly Gly Ser
                165                 170                 175

ttg tca aga aac aat gct caa gta ttg tta tta cct act ttt gca caa   576
Leu Ser Arg Asn Asn Ala Gln Val Leu Leu Leu Pro Thr Phe Ala Gln
            180                 185                 190

gct gca aat gtg cag tta tta cta tta agg gat gca gtt caa tat aaa   624
Ala Ala Asn Val Gln Leu Leu Leu Leu Arg Asp Ala Val Gln Tyr Lys
        195                 200                 205

gca caa tgg ttc cca ttt ttg agt gca gag aat gta aga tcg gaa tta   672
Ala Gln Trp Phe Pro Phe Leu Ser Ala Glu Asn Val Arg Ser Glu Leu
    210                 215                 220

ata tca cct aac agt ggt tgt gat ttt acc ggt gat tac tat gag cga   720
Ile Ser Pro Asn Ser Gly Cys Asp Phe Thr Gly Asp Tyr Tyr Glu Arg
225                 230                 235                 240

tta aaa tgc aaa acg gca gag tat acc aat tat tgt tta tat tgg tat   768
Leu Lys Cys Lys Thr Ala Glu Tyr Thr Asn Tyr Cys Leu Tyr Trp Tyr
                245                 250                 255

cag gta ggt tta aat cag ata aaa cag ggg ggg aca ggt gct gac act   816
Gln Val Gly Leu Asn Gln Ile Lys Gln Gly Gly Thr Gly Ala Asp Thr
            260                 265                 270

tgg tcg aaa ttt aat aaa ttt cgt aga gaa atg acg ttg gcg gta ttg   864
Trp Ser Lys Phe Asn Lys Phe Arg Arg Glu Met Thr Leu Ala Val Leu
        275                 280                 285

gat att atc gct ata ttt cca act tat gat ttt gag aaa tat cca ttg   912
Asp Ile Ile Ala Ile Phe Pro Thr Tyr Asp Phe Glu Lys Tyr Pro Leu
    290                 295                 300

cca aca cat gta gag ttg act agg gaa att tat aca gat gca gtg gga   960
Pro Thr His Val Glu Leu Thr Arg Glu Ile Tyr Thr Asp Ala Val Gly
305                 310                 315                 320

tat tca tcg gga act tat agt tgg tta cgg aat tgg cct aat act ttt   1008
Tyr Ser Ser Gly Thr Tyr Ser Trp Leu Arg Asn Trp Pro Asn Thr Phe
                325                 330                 335

aat ggg tta gag gct aat gga aca cgg gga cct ggt tta gtt act tgg   1056
Asn Gly Leu Glu Ala Asn Gly Thr Arg Gly Pro Gly Leu Val Thr Trp
            340                 345                 350

ctt agc aaa ata ggt ata tat aat gag tat gtt tcg aga tat ttt gcc   1104
Leu Ser Lys Ile Gly Ile Tyr Asn Glu Tyr Val Ser Arg Tyr Phe Ala
        355                 360                 365

ggc tgg gta gga act cgt cat tat gaa gac tac aca aag ggt aac ggt   1152
Gly Trp Val Gly Thr Arg His Tyr Glu Asp Tyr Thr Lys Gly Asn Gly
    370                 375                 380

att ttt caa cgt atg tct gga act acg agt aat gat cta cgt aat att   1200
Ile Phe Gln Arg Met Ser Gly Thr Thr Ser Asn Asp Leu Arg Asn Ile
385                 390                 395                 400

gat ttt cag aat gcc gat gta tat aaa att act tca tta gct atc atg   1248
Asp Phe Gln Asn Ala Asp Val Tyr Lys Ile Thr Ser Leu Ala Ile Met
                405                 410                 415
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aac cta gta gga gag act acc gct aga cca gag tat cgt gtt tca aag   1296
Asn Leu Val Gly Glu Thr Thr Ala Arg Pro Glu Tyr Arg Val Ser Lys
            420                 425                 430

gca gat ttt cgt agg gta ggg gga cct gat tta aat tat gat gca ggt   1344
Ala Asp Phe Arg Arg Val Gly Gly Pro Asp Leu Asn Tyr Asp Ala Gly
        435                 440                 445

aat aat ggg cta agc agg atg aca att gaa tct acg ttc cca ctt gta   1392
Asn Asn Gly Leu Ser Arg Met Thr Ile Glu Ser Thr Phe Pro Leu Val
    450                 455                 460

ttg cac tct aat ggt gtt aga gga ccc tct cat aga tta tca aat gcg   1440
Leu His Ser Asn Gly Val Arg Gly Pro Ser His Arg Leu Ser Asn Ala
465                 470                 475                 480

gca tgt gtt gta tat gga aac tcc aga gtt aac gta tat ggt tgg aca   1488
Ala Cys Val Val Tyr Gly Asn Ser Arg Val Asn Val Tyr Gly Trp Thr
                485                 490                 495

cat aca agt tta aaa cgt gaa aat ata att gaa gcc aat caa att aca   1536
His Thr Ser Leu Lys Arg Glu Asn Ile Ile Glu Ala Asn Gln Ile Thr
            500                 505                 510

caa ata ccg gcg gtg aag agt tat tac ctt caa aat tat ctt gct aat   1584
Gln Ile Pro Ala Val Lys Ser Tyr Tyr Leu Gln Asn Tyr Leu Ala Asn
        515                 520                 525

gcc tat acc tat gta ata aaa ggc act cat aca ggt ggg gat tta atc   1632
Ala Tyr Thr Tyr Val Ile Lys Gly Thr His Thr Gly Gly Asp Leu Ile
    530                 535                 540

cgt ttt tta aga aca aaa tca gag tat aac gca gtt tat gca ggt ggc   1680
Arg Phe Leu Arg Thr Lys Ser Glu Tyr Asn Ala Val Tyr Ala Gly Gly
545                 550                 555                 560

gga att aga ttg att att aat aac aaa act gca gga caa agt tac cgt   1728
Gly Ile Arg Leu Ile Ile Asn Asn Lys Thr Ala Gly Gln Ser Tyr Arg
                565                 570                 575

att cgt ttt cgt tat gct gca gat aaa gct gct ttc ttt agt gta tat   1776
Ile Arg Phe Arg Tyr Ala Ala Asp Lys Ala Ala Phe Phe Ser Val Tyr
            580                 585                 590

ctt tat cca gga ggt tgg ggt tca aat cgt ttt gta tcg ctt gaa aaa   1824
Leu Tyr Pro Gly Gly Trp Gly Ser Asn Arg Phe Val Ser Leu Glu Lys
        595                 600                 605

tct tac tct gga aat tat gac gat tta aaa tat agt gat ttt aaa ttc   1872
Ser Tyr Ser Gly Asn Tyr Asp Asp Leu Lys Tyr Ser Asp Phe Lys Phe
    610                 615                 620

gct gaa att atc aca cct cca tta cct agt tca aac att cag atg gat   1920
Ala Glu Ile Ile Thr Pro Pro Leu Pro Ser Ser Asn Ile Gln Met Asp
625                 630                 635                 640

gtg gag atg caa gcg aat agt ttt caa tca gat gta aac gtg gtt ctc   1968
Val Glu Met Gln Ala Asn Ser Phe Gln Ser Asp Val Asn Val Val Leu
                645                 650                 655

gac aaa att gaa ttc ctc cca agt aat aca aca act tta gaa tat gag   2016
Asp Lys Ile Glu Phe Leu Pro Ser Asn Thr Thr Thr Leu Glu Tyr Glu
            660                 665                 670

gga gaa cgg gac cta gaa aaa aca aag aac gcg gtg aac gat ctg ttt   2064
Gly Glu Arg Asp Leu Glu Lys Thr Lys Asn Ala Val Asn Asp Leu Phe
        675                 680                 685
```

```
acc aat taa                                                          2073
Thr Asn  *
    690


<210> 16
<211> 690
<212> PRT
<213> Bacillus thuringiensis

<400> 16
Met Ser Pro Tyr Gln Asn Lys Asn Glu Tyr Glu Ile Leu Glu Ser Ser
 1               5                  10                  15
Ser Asn Asn Thr Asn Thr Pro Asn Arg Tyr Pro Phe Ala Asn Asn Arg
            20                  25                  30
Asp Met Ser Thr Met Ser Trp Asn Asp Cys Gln Gly Ile Ser Trp Asp
        35                  40                  45
Glu Ile Trp Glu Ser Val Glu Thr Ile Thr Ser Ile Gly Ile Asn Leu
    50                  55                  60
Ile Glu Phe Val Ile Glu Pro Ser Leu Gly Gly Ile Asn Thr Leu Leu
65                  70                  75                  80
Ser Ile Ile Gly Lys Leu Ile Pro Thr Asn Arg Gln Thr Val Ser Ala
                85                  90                  95
Leu Ser Ile Cys Asp Leu Leu Ser Ile Ile Arg Lys Glu Val Ala Asp
            100                 105                 110
Ser Val Leu Ser Asp Ala Ile Ala Asp Phe Asp Gly Lys Leu Lys Asn
        115                 120                 125
Tyr Arg Glu Tyr Tyr Leu Ser Tyr Leu Gly Ala Trp Leu Lys Asp Gly
    130                 135                 140
Lys Pro Leu Gln Lys Thr Asn Asn Ser Asp Ile Gly Gln Leu Val Tyr
145                 150                 155                 160
Tyr Phe Lys Leu Ser Glu Arg Asp Phe Asn Glu Ile Leu Gly Gly Ser
                165                 170                 175
Leu Ser Arg Asn Asn Ala Gln Val Leu Leu Leu Pro Thr Phe Ala Gln
            180                 185                 190
Ala Ala Asn Val Gln Leu Leu Leu Leu Arg Asp Ala Val Gln Tyr Lys
        195                 200                 205
Ala Gln Trp Phe Pro Phe Leu Ser Ala Glu Asn Val Arg Ser Glu Leu
    210                 215                 220
Ile Ser Pro Asn Ser Gly Cys Asp Phe Thr Gly Asp Tyr Tyr Glu Arg
225                 230                 235                 240
Leu Lys Cys Lys Thr Ala Glu Tyr Thr Asn Tyr Cys Leu Tyr Trp Tyr
                245                 250                 255
Gln Val Gly Leu Asn Gln Ile Lys Gln Gly Gly Thr Gly Ala Asp Thr
            260                 265                 270
Trp Ser Lys Phe Asn Lys Phe Arg Arg Glu Met Thr Leu Ala Val Leu
        275                 280                 285
Asp Ile Ile Ala Ile Phe Pro Thr Tyr Asp Phe Glu Lys Tyr Pro Leu
    290                 295                 300
Pro Thr His Val Glu Leu Thr Arg Glu Ile Tyr Thr Asp Ala Val Gly
305                 310                 315                 320
Tyr Ser Ser Gly Thr Tyr Ser Trp Leu Arg Asn Trp Pro Asn Thr Phe
                325                 330                 335
Asn Gly Leu Glu Ala Asn Gly Thr Arg Gly Pro Gly Leu Val Thr Trp
            340                 345                 350
Leu Ser Lys Ile Gly Ile Tyr Asn Glu Tyr Val Ser Arg Tyr Phe Ala
        355                 360                 365
Gly Trp Val Gly Thr Arg His Tyr Glu Asp Tyr Thr Lys Gly Asn Gly
    370                 375                 380
Ile Phe Gln Arg Met Ser Gly Thr Thr Ser Asn Asp Leu Arg Asn Ile
385                 390                 395                 400
Asp Phe Gln Asn Ala Asp Val Tyr Lys Ile Thr Ser Leu Ala Ile Met
                405                 410                 415
Asn Leu Val Gly Glu Thr Thr Ala Arg Pro Glu Tyr Arg Val Ser Lys
            420                 425                 430
Ala Asp Phe Arg Arg Val Gly Gly Pro Asp Leu Asn Tyr Asp Ala Gly
        435                 440                 445
```

```
Asn Asn Gly Leu Ser Arg Met Thr Ile Glu Ser Thr Phe Pro Leu Val
    450                 455                 460
Leu His Ser Asn Gly Val Arg Gly Pro Ser His Arg Leu Ser Asn Ala
465                 470                 475                 480
Ala Cys Val Val Tyr Gly Asn Ser Arg Val Asn Val Tyr Gly Trp Thr
                485                 490                 495
His Thr Ser Leu Lys Arg Glu Asn Ile Ile Glu Ala Asn Gln Ile Thr
            500                 505                 510
Gln Ile Pro Ala Val Lys Ser Tyr Tyr Leu Gln Asn Tyr Leu Ala Asn
        515                 520                 525
Ala Tyr Thr Tyr Val Ile Lys Gly Thr His Thr Gly Gly Asp Leu Ile
    530                 535                 540
Arg Phe Leu Arg Thr Lys Ser Glu Tyr Asn Ala Val Tyr Ala Gly Gly
545                 550                 555                 560
Gly Ile Arg Leu Ile Ile Asn Asn Lys Thr Ala Gly Gln Ser Tyr Arg
                565                 570                 575
Ile Arg Phe Arg Tyr Ala Ala Asp Lys Ala Ala Phe Phe Ser Val Tyr
            580                 585                 590
Leu Tyr Pro Gly Gly Trp Gly Ser Asn Arg Phe Val Ser Leu Glu Lys
        595                 600                 605
Ser Tyr Ser Gly Asn Tyr Asp Asp Leu Lys Tyr Ser Asp Phe Lys Phe
    610                 615                 620
Ala Glu Ile Ile Thr Pro Pro Leu Pro Ser Ser Asn Ile Gln Met Asp
625                 630                 635                 640
Val Glu Met Gln Ala Asn Ser Phe Gln Ser Asp Val Asn Val Val Leu
                645                 650                 655
Asp Lys Ile Glu Phe Leu Pro Ser Asn Thr Thr Thr Leu Glu Tyr Glu
            660                 665                 670
Gly Glu Arg Asp Leu Glu Lys Thr Lys Asn Ala Val Asn Asp Leu Phe
        675                 680                 685
Thr Asn
    690
```

<210> 17
<211> 1686
<212> DNA
<213> Bacillus thuringiensis

<220>
<221> CDS
<222> (1)...(1686)

<400> 17

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gtg agt cct atg ttt aca agt agt acg aaa aat acg tta aaa ata gaa   48
Met Ser Pro Met Phe Thr Ser Ser Thr Lys Asn Thr Leu Lys Ile Glu
 1               5                  10                  15

acg aca gat tat gaa ata gat caa gcg gcc att tct ata gaa tgt atg   96
Thr Thr Asp Tyr Glu Ile Asp Gln Ala Ala Ile Ser Ile Glu Cys Met
            20                  25                  30

tca gat gaa caa aat cct cag gaa aaa ata atg tta tgg gat gaa ata   144
Ser Asp Glu Gln Asn Pro Gln Glu Lys Ile Met Leu Trp Asp Glu Ile
        35                  40                  45

aaa ctg gca aaa caa ctt agt cag tct cgt aat cta ctc caa aat gga   192
Lys Leu Ala Lys Gln Leu Ser Gln Ser Arg Asn Leu Leu Gln Asn Gly
    50                  55                  60

gac ttt tct ggg aat gat tgg aca ttc ggt aat gat att atc ata gga   240
Asp Phe Ser Gly Asn Asp Trp Thr Phe Gly Asn Asp Ile Ile Ile Gly
65                  70                  75                  80

tcc aat aat cct att ttt aaa gga aaa ttt cta cag atg cgt gga gca   288
Ser Asn Asn Pro Ile Phe Lys Gly Lys Phe Leu Gln Met Arg Gly Ala
                85                  90                  95
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```
cga gac ata tat gga act cta ttt cca acc tat atc tgt caa aaa ata   336
Arg Asp Ile Tyr Gly Thr Leu Phe Pro Thr Tyr Ile Cys Gln Lys Ile
            100                 105                 110

gat gag tct aaa tta aaa cca tat aca cgt tat cga gta aga ggg ttt   384
Asp Glu Ser Lys Leu Lys Pro Tyr Thr Arg Tyr Arg Val Arg Gly Phe
        115                 120                 125

gtg gga agt agt aaa gat ttg aaa tta atg gta aca cgt tac ggg aaa   432
Val Gly Ser Ser Lys Asp Leu Lys Leu Met Val Thr Arg Tyr Gly Lys
    130                 135                 140

gaa att gat gct atc atg aat gtt cca aat gat ttg gcc tat atg cag   480
Glu Ile Asp Ala Ile Met Asn Val Pro Asn Asp Leu Ala Tyr Met Gln
145                 150                 155                 160

cct aat cct tca tgt gga gat tat cgc tgt gaa tca tcg tct cag tat   528
Pro Asn Pro Ser Cys Gly Asp Tyr Arg Cys Glu Ser Ser Ser Gln Tyr
                165                 170                 175

gtg agc caa ggg tat cct aca cca aca gat gga tat gct ccc gat atg   576
Val Ser Gln Gly Tyr Pro Thr Pro Thr Asp Gly Tyr Ala Pro Asp Met
            180                 185                 190

tat gca tgc ccg caa aat ata gat aga aag cat gtg aag tgt cac gat   624
Tyr Ala Cys Pro Gln Asn Ile Asp Arg Lys His Val Lys Cys His Asp
        195                 200                 205

cgt cat cca ttt gat ttt cat att gac acc gga gaa gta gat aca aat   672
Arg His Pro Phe Asp Phe His Ile Asp Thr Gly Glu Val Asp Thr Asn
    210                 215                 220

aca aat gta ggt att gat gtc tta tta aaa att tct aat cca gat gga   720
Thr Asn Val Gly Ile Asp Val Leu Leu Lys Ile Ser Asn Pro Asp Gly
225                 230                 235                 240

tac gct aca gta ggg aat cta gaa gtc att gaa gaa gga cca cta aca   768
Tyr Ala Thr Val Gly Asn Leu Glu Val Ile Glu Glu Gly Pro Leu Thr
                245                 250                 255

ggt gaa gca ttg gca cat gtg aaa caa aag gaa aag aaa tgg aaa caa   816
Gly Glu Ala Leu Ala His Val Lys Gln Lys Glu Lys Lys Trp Lys Gln
            260                 265                 270

cac atg gag aaa aaa cgt tgg gaa aca caa caa gcc tat gat cca gca   864
His Met Glu Lys Lys Arg Trp Glu Thr Gln Gln Ala Tyr Asp Pro Ala
        275                 280                 285

aaa cag gct gta gat gca tta ttt aca aat gaa caa gag tta cac tat   912
Lys Gln Ala Val Asp Ala Leu Phe Thr Asn Glu Gln Glu Leu His Tyr
    290                 295                 300

cat att act tta gat cat att caa aac gct gat cga ctg gta cag tcg   960
His Ile Thr Leu Asp His Ile Gln Asn Ala Asp Arg Leu Val Gln Ser
305                 310                 315                 320

att ccc tat gta tac cat aat tgg tta ccg aat gct cca ggt atg aac   1008
Ile Pro Tyr Val Tyr His Asn Trp Leu Pro Asn Ala Pro Gly Met Asn
                325                 330                 335

tat gat gta tat caa gag tta aac gca cgt atc atg caa ggt tat aat   1056
Tyr Asp Val Tyr Gln Glu Leu Asn Ala Arg Ile Met Gln Gly Tyr Asn
            340                 345                 350

tta tat gat gca cga aat gtc ata aca aat ggt gac ttt aca caa gga   1104
Leu Tyr Asp Ala Arg Asn Val Ile Thr Asn Gly Asp Phe Thr Gln Gly
        355                 360                 365
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tta cag gga tgg cac gca aca gga aat gcc gcg gta caa caa atg gat   1152
Leu Gln Gly Trp His Ala Thr Gly Asn Ala Ala Val Gln Gln Met Asp
    370                 375                 380

gga gct tca gta tta gtt cta tca aat tgg agc gcg ggg gta tct caa   1200
Gly Ala Ser Val Leu Val Leu Ser Asn Trp Ser Ala Gly Val Ser Gln
385                 390                 395                 400

aac ttg cat gct caa gat cat cat gga tat gtg tta cgt gtg att gcc   1248
Asn Leu His Ala Gln Asp His His Gly Tyr Val Leu Arg Val Ile Ala
                405                 410                 415

aaa aaa gaa gga cct gga aaa ggg tat gta acg atg atg gat tgt aat   1296
Lys Lys Glu Gly Pro Gly Lys Gly Tyr Val Thr Met Met Asp Cys Asn
            420                 425                 430

gga aag cag gaa aca ctt aag ttc act tct tgc gaa gaa gga tat atg   1344
Gly Lys Gln Glu Thr Leu Lys Phe Thr Ser Cys Glu Glu Gly Tyr Met
        435                 440                 445

aca aaa aca gta gag gta ttc cca gaa agt gat cgt gta cgg att gaa   1392
Thr Lys Thr Val Glu Val Phe Pro Glu Ser Asp Arg Val Arg Ile Glu
    450                 455                 460

ata gga gaa acc gaa ggt aca ttt tat ata gat agc atc gag ttg ctt   1440
Ile Gly Glu Thr Glu Gly Thr Phe Tyr Ile Asp Ser Ile Glu Leu Leu
465                 470                 475                 480

tgt atg caa gga tat gat aac aat aat aac ctg cac acg ggt aat atg   1488
Cys Met Gln Gly Tyr Asp Asn Asn Asn Asn Leu His Thr Gly Asn Met
                485                 490                 495

tat gag caa agt tat aat gga aat tat aat caa aat act agc gat gtg   1536
Tyr Glu Gln Ser Tyr Asn Gly Asn Tyr Asn Gln Asn Thr Ser Asp Val
            500                 505                 510

tat tac caa ggg tat aca aac aac tat aac caa gac tct agt aat atg   1584
Tyr Tyr Gln Gly Tyr Thr Asn Asn Tyr Asn Gln Asp Ser Ser Asn Met
        515                 520                 525

tat aat caa aat tat act aac aat gat gac ctg cat tcc ggt tgc aca   1632
Tyr Asn Gln Asn Tyr Thr Asn Asn Asp Asp Leu His Ser Gly Cys Thr
    530                 535                 540

tgt aac caa ggg cat aac tct ggc tgt aca tgt aat caa gga tat aac   1680
Cys Asn Gln Gly His Asn Ser Gly Cys Thr Cys Asn Gln Gly Tyr Asn
545                 550                 555                 560

cgt taa                                                         1686
Arg  *
```

<210> 18
<211> 561
<212> PRT
<213> Bacillus thuringiensis

<400> 18

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Met Ser Pro Met Phe Thr Ser Ser Thr Lys Asn Thr Leu Lys Ile Glu
 1               5                  10                  15
Thr Thr Asp Tyr Glu Ile Asp Gln Ala Ala Ile Ser Ile Glu Cys Met
            20                  25                  30
Ser Asp Glu Gln Asn Pro Gln Glu Lys Ile Met Leu Trp Asp Glu Ile
        35                  40                  45
Lys Leu Ala Lys Gln Leu Ser Gln Ser Arg Asn Leu Leu Gln Asn Gly
    50                  55                  60
Asp Phe Ser Gly Asn Asp Trp Thr Phe Gly Asn Asp Ile Ile Ile Gly
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65                  70                  75                  80
Ser Asn Asn Pro Ile Phe Lys Gly Lys Phe Leu Gln Met Arg Gly Ala
                85                  90                  95
Arg Asp Ile Tyr Gly Thr Leu Phe Pro Thr Tyr Ile Cys Gln Lys Ile
            100                 105                 110
Asp Glu Ser Lys Leu Lys Pro Tyr Thr Arg Tyr Arg Val Arg Gly Phe
        115                 120                 125
Val Gly Ser Ser Lys Asp Leu Lys Leu Met Val Thr Arg Tyr Gly Lys
    130                 135                 140
Glu Ile Asp Ala Ile Met Asn Val Pro Asn Asp Leu Ala Tyr Met Gln
145                 150                 155                 160
Pro Asn Pro Ser Cys Gly Asp Tyr Arg Cys Glu Ser Ser Ser Gln Tyr
                165                 170                 175
Val Ser Gln Gly Tyr Pro Thr Pro Thr Asp Gly Tyr Ala Pro Asp Met
            180                 185                 190
Tyr Ala Cys Pro Gln Asn Ile Asp Arg Lys His Val Lys Cys His Asp
        195                 200                 205
Arg His Pro Phe Asp Phe His Ile Asp Thr Gly Glu Val Asp Thr Asn
    210                 215                 220
Thr Asn Val Gly Ile Asp Val Leu Leu Lys Ile Ser Asn Pro Asp Gly
225                 230                 235                 240
Tyr Ala Thr Val Gly Asn Leu Glu Val Ile Glu Glu Gly Pro Leu Thr
                245                 250                 255
Gly Glu Ala Leu Ala His Val Lys Gln Lys Glu Lys Lys Trp Lys Gln
            260                 265                 270
His Met Glu Lys Lys Arg Trp Glu Thr Gln Gln Ala Tyr Asp Pro Ala
        275                 280                 285
Lys Gln Ala Val Asp Ala Leu Phe Thr Asn Glu Gln Glu Leu His Tyr
    290                 295                 300
His Ile Thr Leu Asp His Ile Gln Asn Ala Asp Arg Leu Val Gln Ser
305                 310                 315                 320
Ile Pro Tyr Val Tyr His Asn Trp Leu Pro Asn Ala Pro Gly Met Asn
                325                 330                 335
Tyr Asp Val Tyr Gln Glu Leu Asn Ala Arg Ile Met Gln Gly Tyr Asn
            340                 345                 350
Leu Tyr Asp Ala Arg Asn Val Ile Thr Asn Gly Asp Phe Thr Gln Gly
        355                 360                 365
Leu Gln Gly Trp His Ala Thr Gly Asn Ala Ala Val Gln Gln Met Asp
    370                 375                 380
Gly Ala Ser Val Leu Val Leu Ser Asn Trp Ser Ala Gly Val Ser Gln
385                 390                 395                 400
Asn Leu His Ala Gln Asp His His Gly Tyr Val Leu Arg Val Ile Ala
                405                 410                 415
Lys Lys Glu Gly Pro Gly Lys Gly Tyr Val Thr Met Met Asp Cys Asn
            420                 425                 430
Gly Lys Gln Glu Thr Leu Lys Phe Thr Ser Cys Glu Glu Gly Tyr Met
        435                 440                 445
Thr Lys Thr Val Glu Val Phe Pro Glu Ser Asp Arg Val Arg Ile Glu
    450                 455                 460
Ile Gly Glu Thr Glu Gly Thr Phe Tyr Ile Asp Ser Ile Glu Leu Leu
465                 470                 475                 480
Cys Met Gln Gly Tyr Asp Asn Asn Asn Asn Leu His Thr Gly Asn Met
                485                 490                 495
Tyr Glu Gln Ser Tyr Asn Gly Asn Tyr Asn Gln Asn Thr Ser Asp Val
            500                 505                 510
Tyr Tyr Gln Gly Tyr Thr Asn Asn Tyr Asn Gln Asp Ser Ser Asn Met
        515                 520                 525
Tyr Asn Gln Asn Tyr Thr Asn Asn Asp Asp Leu His Ser Gly Cys Thr
    530                 535                 540
Cys Asn Gln Gly His Asn Ser Gly Cys Thr Cys Asn Gln Gly Tyr Asn
545                 550                 555                 560
Arg
```

<210> 19
<211> 2049
<212> DNA

<213> Bacillus thuringiensis

<220>
<221> CDS
<222> (1)...(2049)

<400> 19

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atg aat tca tat aaa aat aaa aat gaa tat gaa atg ttg gat gct tta   48
Met Asn Ser Tyr Lys Asn Lys Asn Glu Tyr Glu Met Leu Asp Ala Leu
 1               5                  10                  15

cga atc aac tct aat atg tct aat tgt tat cca agg tat cca cta gca   96
Arg Ile Asn Ser Asn Met Ser Asn Cys Tyr Pro Arg Tyr Pro Leu Ala
            20                  25                  30

aaa gat cca caa atg act atg cga aac acg aac tat aaa gaa tgg cta   144
Lys Asp Pro Gln Met Thr Met Arg Asn Thr Asn Tyr Lys Glu Trp Leu
        35                  40                  45

aat atg tgt gat tca aat aca caa ttt att ggt gat ata agc acg tat   192
Asn Met Cys Asp Ser Asn Thr Gln Phe Ile Gly Asp Ile Ser Thr Tyr
    50                  55                  60

tct agc cct gaa gct gct tta agt gta cga gat gct gtt tta acg ggt   240
Ser Ser Pro Glu Ala Ala Leu Ser Val Arg Asp Ala Val Leu Thr Gly
65                  70                  75                  80

att aac agt gta ggg act ata ctt tcg aat tta ggg gtc cct ttg gca   288
Ile Asn Ser Val Gly Thr Ile Leu Ser Asn Leu Gly Val Pro Leu Ala
                85                  90                  95

agt caa tca ttt gga ata att agt agg cta ata ggt att tta tgg gca   336
Ser Gln Ser Phe Gly Ile Ile Ser Arg Leu Ile Gly Ile Leu Trp Ala
            100                 105                 110

ggg cct gat cca ttt gaa gca ctt atg gtt ctt gtt gaa gag ctt att   384
Gly Pro Asp Pro Phe Glu Ala Leu Met Val Leu Val Glu Glu Leu Ile
        115                 120                 125

aag aaa agt ata gat cag cgt gta aga gaa aat gct ctt aga gag cta   432
Lys Lys Ser Ile Asp Gln Arg Val Arg Glu Asn Ala Leu Arg Glu Leu
    130                 135                 140

gaa ggt tta cag gga att atg aga cta tat caa act aga ctg caa gca   480
Glu Gly Leu Gln Gly Ile Met Arg Leu Tyr Gln Thr Arg Leu Gln Ala
145                 150                 155                 160

tgg cta gtt aac aag aat gat gac aat cgg agg gca cta gta acg cag   528
Trp Leu Val Asn Lys Asn Asp Asp Asn Arg Arg Ala Leu Val Thr Gln
                165                 170                 175

tat gca att gtt gat aac ttt ttc gaa aag aat atg cca aaa ttc aag   576
Tyr Ala Ile Val Asp Asn Phe Phe Glu Lys Asn Met Pro Lys Phe Lys
            180                 185                 190

gaa aga aac ttt gaa att tta ttg tta cca gta tat gca caa gcc gcg   624
Glu Arg Asn Phe Glu Ile Leu Leu Leu Pro Val Tyr Ala Gln Ala Ala
        195                 200                 205

aat ttg cat tta att tta tta aga gat gct gat tat ttt gga gca cag   672
Asn Leu His Leu Ile Leu Leu Arg Asp Ala Asp Tyr Phe Gly Ala Gln
    210                 215                 220

tgg caa tta ggt gat gat gaa att cgt gat aat tat atc aga cta caa   720
Trp Gln Leu Gly Asp Asp Glu Ile Arg Asp Asn Tyr Ile Arg Leu Gln
225                 230                 235                 240

gga ctg att aga gaa tat aaa gat cat tgt ata aca ttc tat aac cag   768
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```
Gly Leu Ile Arg Glu Tyr Lys Asp His Cys Ile Thr Phe Tyr Asn Gln
                245                 250                 255

ggt tta aat caa ttt aat cgc tca aat gct caa gat tgg gtg agc ttt   816
Gly Leu Asn Gln Phe Asn Arg Ser Asn Ala Gln Asp Trp Val Ser Phe
            260                 265                 270

aat agg ttt cgt aca gat atg aca tta aca gta tta gat ctc gca ata   864
Asn Arg Phe Arg Thr Asp Met Thr Leu Thr Val Leu Asp Leu Ala Ile
        275                 280                 285

tta ttt cca aac tat gat cca cgt agg tat cca tta gca gta aaa acg   912
Leu Phe Pro Asn Tyr Asp Pro Arg Arg Tyr Pro Leu Ala Val Lys Thr
    290                 295                 300

gaa ttg act agg gaa gtt tat aca gat cca gta ggg ttt act ggg gta   960
Glu Leu Thr Arg Glu Val Tyr Thr Asp Pro Val Gly Phe Thr Gly Val
305                 310                 315                 320

tta gaa agt gga ggt agg act tac cct tgg tat aat cct aat aat aca   1008
Leu Glu Ser Gly Gly Arg Thr Tyr Pro Trp Tyr Asn Pro Asn Asn Thr
                325                 330                 335

acc ttt act gct atg gaa aat aac gca aga cga cgt cct tct tat acc   1056
Thr Phe Thr Ala Met Glu Asn Asn Ala Arg Arg Arg Pro Ser Tyr Thr
            340                 345                 350

act tgg ctt aat cgt att ttt gta tat aca agg act cta ggt aat atg   1104
Thr Trp Leu Asn Arg Ile Phe Val Tyr Thr Arg Thr Leu Gly Asn Met
        355                 360                 365

tct gat gtg aga aat att tgg gga ggg cat aca tta gtt gaa aat gga   1152
Ser Asp Val Arg Asn Ile Trp Gly Gly His Thr Leu Val Glu Asn Gly
    370                 375                 380

aat gat ggt tct gaa ata acc cat aac ttt ggt aaa act gat tct att   1200
Asn Asp Gly Ser Glu Ile Thr His Asn Phe Gly Lys Thr Asp Ser Ile
385                 390                 395                 400

act cct att caa tat ttt aat ttc gcg aac ctt tct gtt ttc agt att   1248
Thr Pro Ile Gln Tyr Phe Asn Phe Ala Asn Leu Ser Val Phe Ser Ile
                405                 410                 415

gag tca ctt gct cgt ata tat tta gga gga aca gag gct aat aat tat   1296
Glu Ser Leu Ala Arg Ile Tyr Leu Gly Gly Thr Glu Ala Asn Asn Tyr
            420                 425                 430

att act agt cag tat gga gtc tcg aga gtt att ttt aat aca tca aat   1344
Ile Thr Ser Gln Tyr Gly Val Ser Arg Val Ile Phe Asn Thr Ser Asn
        435                 440                 445

ata aat aat gta cct gga tct tta aga tac gaa gtg cct gct aat ctt   1392
Ile Asn Asn Val Pro Gly Ser Leu Arg Tyr Glu Val Pro Ala Asn Leu
    450                 455                 460

cca tcc caa act ata tta tca gaa tta cca gga aag gat aag cca aga   1440
Pro Ser Gln Thr Ile Leu Ser Glu Leu Pro Gly Lys Asp Lys Pro Arg
465                 470                 475                 480

cca aac gca gga gat ttc agc cat aga tta tct tat ata tca aat ttt   1488
Pro Asn Ala Gly Asp Phe Ser His Arg Leu Ser Tyr Ile Ser Asn Phe
                485                 490                 495

gat gca cgg cga agt agt tca ggc ggt att gtt agt ctt tta acg ttt   1536
Asp Ala Arg Arg Ser Ser Ser Gly Gly Ile Val Ser Leu Leu Thr Phe
            500                 505                 510

ggt tgg gca cat acc agt atg gat cgt aat aat cgt ctt gaa cca gat   1584
```

```
Gly Trp Ala His Thr Ser Met Asp Arg Asn Asn Arg Leu Glu Pro Asp
        515                 520                 525

aaa att act caa ata gat gca gtt aaa ggt tgg ggg ggg aat atc ggg   1632
Lys Ile Thr Gln Ile Asp Ala Val Lys Gly Trp Gly Gly Asn Ile Gly
    530                 535                 540

ttt gtc atc cca gga cct act ggg ggg aat ttg gta aaa gtc agt gat   1680
Phe Val Ile Pro Gly Pro Thr Gly Gly Asn Leu Val Lys Val Ser Asp
545                 550                 555                 560

agt tgg cat tca ctt aaa gtt caa gca cca caa aga caa aca agt tat   1728
Ser Trp His Ser Leu Lys Val Gln Ala Pro Gln Arg Gln Thr Ser Tyr
                565                 570                 575

cgt att cgt ttg cgt tat gct tgt tta gtt acc cat ggg gat gct att   1776
Arg Ile Arg Leu Arg Tyr Ala Cys Leu Val Thr His Gly Asp Ala Ile
            580                 585                 590

ttt gta gaa cac agc ggc agt agt cat ata gtt tca ttt ttt gat tgc   1824
Phe Val Glu His Ser Gly Ser Ser His Ile Val Ser Phe Phe Asp Cys
        595                 600                 605

tca aat tca tca ggt cgt cca tca aac act ctt cta gag agt gat ttt   1872
Ser Asn Ser Ser Gly Arg Pro Ser Asn Thr Leu Leu Glu Ser Asp Phe
    610                 615                 620

cgc tat att gat gtt cca ggt att ttt aca cca tca ata aat ccc tta   1920
Arg Tyr Ile Asp Val Pro Gly Ile Phe Thr Pro Ser Ile Asn Pro Leu
625                 630                 635                 640

ata aga tat aga aca caa agc ttt ggt acc cac gcg ata gac aaa ttt   1968
Ile Arg Tyr Arg Thr Gln Ser Phe Gly Thr His Ala Ile Asp Lys Phe
                645                 650                 655

gaa ttt att cca ctt aac act ttt ccg aat caa tca tta gaa aaa aga   2016
Glu Phe Ile Pro Leu Asn Thr Phe Pro Asn Gln Ser Leu Glu Lys Arg
            660                 665                 670

gaa cag gaa gta aat gat cta ttt atc aat taa                      2049
Glu Gln Glu Val Asn Asp Leu Phe Ile Asn  *
        675                 680
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<210> 20
<211> 682
<212> PRT
<213> Bacillus thuringiensis

<400> 20

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Met Asn Ser Tyr Lys Asn Lys Asn Glu Tyr Glu Met Leu Asp Ala Leu
 1               5                  10                  15
Arg Ile Asn Ser Asn Met Ser Asn Cys Tyr Pro Arg Tyr Pro Leu Ala
            20                  25                  30
Lys Asp Pro Gln Met Thr Met Arg Asn Thr Asn Tyr Lys Glu Trp Leu
        35                  40                  45
Asn Met Cys Asp Ser Asn Thr Gln Phe Ile Gly Asp Ile Ser Thr Tyr
    50                  55                  60
Ser Ser Pro Glu Ala Ala Leu Ser Val Arg Asp Ala Val Leu Thr Gly
65                  70                  75                  80
Ile Asn Ser Val Gly Thr Ile Leu Ser Asn Leu Gly Val Pro Leu Ala
                85                  90                  95
Ser Gln Ser Phe Gly Ile Ile Ser Arg Leu Ile Gly Ile Leu Trp Ala
            100                 105                 110
Gly Pro Asp Pro Phe Glu Ala Leu Met Val Leu Val Glu Glu Leu Ile
        115                 120                 125
Lys Lys Ser Ile Asp Gln Arg Val Arg Glu Asn Ala Leu Arg Glu Leu
    130                 135                 140
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Glu Gly Leu Gln Gly Ile Met Arg Leu Tyr Gln Thr Arg Leu Gln Ala
145                 150                 155                 160
Trp Leu Val Asn Lys Asn Asp Asp Asn Arg Arg Ala Leu Val Thr Gln
                165                 170                 175
Tyr Ala Ile Val Asp Asn Phe Phe Glu Lys Asn Met Pro Lys Phe Lys
            180                 185                 190
Glu Arg Asn Phe Glu Ile Leu Leu Leu Pro Val Tyr Ala Gln Ala Ala
        195                 200                 205
Asn Leu His Leu Ile Leu Leu Arg Asp Ala Asp Tyr Phe Gly Ala Gln
    210                 215                 220
Trp Gln Leu Gly Asp Asp Glu Ile Arg Asp Asn Tyr Ile Arg Leu Gln
225                 230                 235                 240
Gly Leu Ile Arg Glu Tyr Lys Asp His Cys Ile Thr Phe Tyr Asn Gln
                245                 250                 255
Gly Leu Asn Gln Phe Asn Arg Ser Asn Ala Gln Asp Trp Val Ser Phe
            260                 265                 270
Asn Arg Phe Arg Thr Asp Met Thr Leu Thr Val Leu Asp Leu Ala Ile
        275                 280                 285
Leu Phe Pro Asn Tyr Asp Pro Arg Arg Tyr Pro Leu Ala Val Lys Thr
    290                 295                 300
Glu Leu Thr Arg Glu Val Tyr Thr Asp Pro Val Gly Phe Thr Gly Val
305                 310                 315                 320
Leu Glu Ser Gly Gly Arg Thr Tyr Pro Trp Tyr Asn Pro Asn Asn Thr
                325                 330                 335
Thr Phe Thr Ala Met Glu Asn Asn Ala Arg Arg Arg Pro Ser Tyr Thr
            340                 345                 350
Thr Trp Leu Asn Arg Ile Phe Val Tyr Thr Arg Thr Leu Gly Asn Met
        355                 360                 365
Ser Asp Val Arg Asn Ile Trp Gly Gly His Thr Leu Val Glu Asn Gly
    370                 375                 380
Asn Asp Gly Ser Glu Ile Thr His Asn Phe Gly Lys Thr Asp Ser Ile
385                 390                 395                 400
Thr Pro Ile Gln Tyr Phe Asn Phe Ala Asn Leu Ser Val Phe Ser Ile
                405                 410                 415
Glu Ser Leu Ala Arg Ile Tyr Leu Gly Gly Thr Glu Ala Asn Asn Tyr
            420                 425                 430
Ile Thr Ser Gln Tyr Gly Val Ser Arg Val Ile Phe Asn Thr Ser Asn
        435                 440                 445
Ile Asn Asn Val Pro Gly Ser Leu Arg Tyr Glu Val Pro Ala Asn Leu
    450                 455                 460
Pro Ser Gln Thr Ile Leu Ser Glu Leu Pro Gly Lys Asp Lys Pro Arg
465                 470                 475                 480
Pro Asn Ala Gly Asp Phe Ser His Arg Leu Ser Tyr Ile Ser Asn Phe
                485                 490                 495
Asp Ala Arg Arg Ser Ser Ser Gly Gly Ile Val Ser Leu Leu Thr Phe
            500                 505                 510
Gly Trp Ala His Thr Ser Met Asp Arg Asn Asn Arg Leu Glu Pro Asp
        515                 520                 525
Lys Ile Thr Gln Ile Asp Ala Val Lys Gly Trp Gly Gly Asn Ile Gly
    530                 535                 540
Phe Val Ile Pro Gly Pro Thr Gly Gly Asn Leu Val Lys Val Ser Asp
545                 550                 555                 560
Ser Trp His Ser Leu Lys Val Gln Ala Pro Gln Arg Gln Thr Ser Tyr
                565                 570                 575
Arg Ile Arg Leu Arg Tyr Ala Cys Leu Val Thr His Gly Asp Ala Ile
            580                 585                 590
Phe Val Glu His Ser Gly Ser Ser His Ile Val Ser Phe Phe Asp Cys
        595                 600                 605
Ser Asn Ser Ser Gly Arg Pro Ser Asn Thr Leu Leu Glu Ser Asp Phe
    610                 615                 620
Arg Tyr Ile Asp Val Pro Gly Ile Phe Thr Pro Ser Ile Asn Pro Leu
625                 630                 635                 640
Ile Arg Tyr Arg Thr Gln Ser Phe Gly Thr His Ala Ile Asp Lys Phe
                645                 650                 655
Glu Phe Ile Pro Leu Asn Thr Phe Pro Asn Gln Ser Leu Glu Lys Arg
            660                 665                 670
Glu Gln Glu Val Asn Asp Leu Phe Ile Asn
        675                 680
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<210> 21
<211> 2016
<212> DNA
<213> Bacillus thuringiensis

<220>
<221> CDS
<222> (1)...(2016)

<400> 21

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atg ttg gat gct tta cga atc aac tct aat atg tct aat tgt tat cca   48
Met Leu Asp Ala Leu Arg Ile Asn Ser Asn Met Ser Asn Cys Tyr Pro
 1               5                  10                  15

agg tat cca cta gca aaa gat cca caa atg act atg cga aac acg aac   96
Arg Tyr Pro Leu Ala Lys Asp Pro Gln Met Thr Met Arg Asn Thr Asn
            20                  25                  30

tat aaa gaa tgg cta aat atg tgt gat tca aat aca caa ttt att ggt   144
Tyr Lys Glu Trp Leu Asn Met Cys Asp Ser Asn Thr Gln Phe Ile Gly
        35                  40                  45

gat ata agc acg tat tct agc cct gaa gct gct tta agt gta cga gat   192
Asp Ile Ser Thr Tyr Ser Ser Pro Glu Ala Ala Leu Ser Val Arg Asp
    50                  55                  60

gct gtt tta acg ggt att aac agt gta ggg act ata ctt tcg aat tta   240
Ala Val Leu Thr Gly Ile Asn Ser Val Gly Thr Ile Leu Ser Asn Leu
65                  70                  75                  80

ggg gtc cct ttg gca agt caa tca ttt gga ata att agt agg cta ata   288
Gly Val Pro Leu Ala Ser Gln Ser Phe Gly Ile Ile Ser Arg Leu Ile
                85                  90                  95

ggt att tta tgg gca ggg cct gat cca ttt gaa gca ctt atg gtt ctt   336
Gly Ile Leu Trp Ala Gly Pro Asp Pro Phe Glu Ala Leu Met Val Leu
            100                 105                 110

gtt gaa gag ctt att aag aaa agt ata gat cag cgt gta aga gaa aat   384
Val Glu Glu Leu Ile Lys Lys Ser Ile Asp Gln Arg Val Arg Glu Asn
        115                 120                 125

gct ctt aga gag cta gaa ggt tta cag gga att atg aga cta tat caa   432
Ala Leu Arg Glu Leu Glu Gly Leu Gln Gly Ile Met Arg Leu Tyr Gln
    130                 135                 140

act aga ctg caa gca tgg cta gtt aac aag aat gat gac aat cgg agg   480
Thr Arg Leu Gln Ala Trp Leu Val Asn Lys Asn Asp Asp Asn Arg Arg
145                 150                 155                 160

gca cta gta acg cag tat gca att gtt gat aac ttt ttc gaa aag aat   528
Ala Leu Val Thr Gln Tyr Ala Ile Val Asp Asn Phe Phe Glu Lys Asn
                165                 170                 175

atg cca aaa ttc aag gaa aga aac ttt gaa att tta ttg tta cca gta   576
Met Pro Lys Phe Lys Glu Arg Asn Phe Glu Ile Leu Leu Leu Pro Val
            180                 185                 190

tat gca caa gcc gcg aat ttg cat tta att tta tta aga gat gct gat   624
Tyr Ala Gln Ala Ala Asn Leu His Leu Ile Leu Leu Arg Asp Ala Asp
        195                 200                 205

tat ttt gga gca cag tgg caa tta ggt gat gat gaa att cgt gat aat   672
Tyr Phe Gly Ala Gln Trp Gln Leu Gly Asp Asp Glu Ile Arg Asp Asn
    210                 215                 220
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tat atc aga cta caa gga ctg att aga gaa tat aaa gat cat tgt ata   720
Tyr Ile Arg Leu Gln Gly Leu Ile Arg Glu Tyr Lys Asp His Cys Ile
225                 230                 235                 240

aca ttc tat aac cag ggt tta aat caa ttt aat cgc tca aat gct caa   768
Thr Phe Tyr Asn Gln Gly Leu Asn Gln Phe Asn Arg Ser Asn Ala Gln
                245                 250                 255

gat tgg gtg agc ttt aat agg ttt cgt aca gat atg aca tta aca gta   816
Asp Trp Val Ser Phe Asn Arg Phe Arg Thr Asp Met Thr Leu Thr Val
            260                 265                 270

tta gat ctc gca ata tta ttt cca aac tat gat cca cgt agg tat cca   864
Leu Asp Leu Ala Ile Leu Phe Pro Asn Tyr Asp Pro Arg Arg Tyr Pro
        275                 280                 285

tta gca gta aaa acg gaa ttg act agg gaa gtt tat aca gat cca gta   912
Leu Ala Val Lys Thr Glu Leu Thr Arg Glu Val Tyr Thr Asp Pro Val
    290                 295                 300

ggg ttt act ggg gta tta gaa agt gga ggt agg act tac cct tgg tat   960
Gly Phe Thr Gly Val Leu Glu Ser Gly Gly Arg Thr Tyr Pro Trp Tyr
305                 310                 315                 320

aat cct aat aat aca acc ttt act gct atg gaa aat aac gca aga cga   1008
Asn Pro Asn Asn Thr Thr Phe Thr Ala Met Glu Asn Asn Ala Arg Arg
                325                 330                 335

cgt cct tct tat acc act tgg ctt aat cgt att ttt gta tat aca agg   1056
Arg Pro Ser Tyr Thr Thr Trp Leu Asn Arg Ile Phe Val Tyr Thr Arg
            340                 345                 350

act cta ggt aat atg tct gat gtg aga aat att tgg gga ggg cat aca   1104
Thr Leu Gly Asn Met Ser Asp Val Arg Asn Ile Trp Gly Gly His Thr
        355                 360                 365

tta gtt gaa aat gga aat gat ggt tct gaa ata acc cat aac ttt ggt   1152
Leu Val Glu Asn Gly Asn Asp Gly Ser Glu Ile Thr His Asn Phe Gly
    370                 375                 380

aaa act gat tct att act cct att caa tat ttt aat ttc gcg aac ctt   1200
Lys Thr Asp Ser Ile Thr Pro Ile Gln Tyr Phe Asn Phe Ala Asn Leu
385                 390                 395                 400

tct gtt ttc agt att gag tca ctt gct cgt ata tat tta gga gga aca   1248
Ser Val Phe Ser Ile Glu Ser Leu Ala Arg Ile Tyr Leu Gly Gly Thr
                405                 410                 415

gag gct aat aat tat att act agt cag tat gga gtc tcg aga gtt att   1296
Glu Ala Asn Asn Tyr Ile Thr Ser Gln Tyr Gly Val Ser Arg Val Ile
            420                 425                 430

ttt aat aca tca aat ata aat aat gta cct gga tct tta aga tac gaa   1344
Phe Asn Thr Ser Asn Ile Asn Asn Val Pro Gly Ser Leu Arg Tyr Glu
        435                 440                 445

gtg cct gct aat ctt cca tcc caa act ata tta tca gaa tta cca gga   1392
Val Pro Ala Asn Leu Pro Ser Gln Thr Ile Leu Ser Glu Leu Pro Gly
    450                 455                 460

aag gat aag cca aga cca aac gca gga gat ttc agc cat aga tta tct   1440
Lys Asp Lys Pro Arg Pro Asn Ala Gly Asp Phe Ser His Arg Leu Ser
465                 470                 475                 480

tat ata tca aat ttt gat gca cgg cga agt agt tca ggc ggt att gtt   1488
Tyr Ile Ser Asn Phe Asp Ala Arg Arg Ser Ser Ser Gly Gly Ile Val
                485                 490                 495
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agt ctt tta acg ttt ggt tgg gca cat acc agt atg gat cgt aat aat   1536
Ser Leu Leu Thr Phe Gly Trp Ala His Thr Ser Met Asp Arg Asn Asn
            500                 505                 510

cgt ctt gaa cca gat aaa att act caa ata gat gca gtt aaa ggt tgg   1584
Arg Leu Glu Pro Asp Lys Ile Thr Gln Ile Asp Ala Val Lys Gly Trp
        515                 520                 525

ggg ggg aat atc ggg ttt gtc atc cca gga cct act ggg ggg aat ttg   1632
Gly Gly Asn Ile Gly Phe Val Ile Pro Gly Pro Thr Gly Gly Asn Leu
    530                 535                 540

gta aaa gtc agt gat agt tgg cat tca ctt aaa gtt caa gca cca caa   1680
Val Lys Val Ser Asp Ser Trp His Ser Leu Lys Val Gln Ala Pro Gln
545                 550                 555                 560

aga caa aca agt tat cgt att cgt ttg cgt tat gct tgt tta gtt acc   1728
Arg Gln Thr Ser Tyr Arg Ile Arg Leu Arg Tyr Ala Cys Leu Val Thr
                565                 570                 575

cat ggg gat gct att ttt gta gaa cac agc ggc agt agt cat ata gtt   1776
His Gly Asp Ala Ile Phe Val Glu His Ser Gly Ser Ser His Ile Val
            580                 585                 590

tca ttt ttt gat tgc tca aat tca tca ggt cgt cca tca aac act ctt   1824
Ser Phe Phe Asp Cys Ser Asn Ser Ser Gly Arg Pro Ser Asn Thr Leu
        595                 600                 605

cta gag agt gat ttt cgc tat att gat gtt cca ggt att ttt aca cca   1872
Leu Glu Ser Asp Phe Arg Tyr Ile Asp Val Pro Gly Ile Phe Thr Pro
    610                 615                 620

tca ata aat ccc tta ata aga tat aga aca caa agc ttt ggt acc cac   1920
Ser Ile Asn Pro Leu Ile Arg Tyr Arg Thr Gln Ser Phe Gly Thr His
625                 630                 635                 640

gcg ata gac aaa ttt gaa ttt att cca ctt aac act ttt ccg aat caa   1968
Ala Ile Asp Lys Phe Glu Phe Ile Pro Leu Asn Thr Phe Pro Asn Gln
                645                 650                 655

tca tta gaa aaa aga gaa cag gaa gta aat gat cta ttt atc aat taa   2016
Ser Leu Glu Lys Arg Glu Gln Glu Val Asn Asp Leu Phe Ile Asn  *
            660                 665                 670
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<210> 22
<211> 671
<212> PRT
<213> Bacillus thuringiensis

<400> 22

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Met Leu Asp Ala Leu Arg Ile Asn Ser Asn Met Ser Asn Cys Tyr Pro
 1               5                  10                  15
Arg Tyr Pro Leu Ala Lys Asp Pro Gln Met Thr Met Arg Asn Thr Asn
            20                  25                  30
Tyr Lys Glu Trp Leu Asn Met Cys Asp Ser Asn Thr Gln Phe Ile Gly
        35                  40                  45
Asp Ile Ser Thr Tyr Ser Ser Pro Glu Ala Ala Leu Ser Val Arg Asp
    50                  55                  60
Ala Val Leu Thr Gly Ile Asn Ser Val Gly Thr Ile Leu Ser Asn Leu
65                  70                  75                  80
Gly Val Pro Leu Ala Ser Gln Ser Phe Gly Ile Ile Ser Arg Leu Ile
                85                  90                  95
Gly Ile Leu Trp Ala Gly Pro Asp Pro Phe Glu Ala Leu Met Val Leu
            100                 105                 110
Val Glu Glu Leu Ile Lys Lys Ser Ile Asp Gln Arg Val Arg Glu Asn
        115                 120                 125
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Ala Leu Arg Glu Leu Glu Gly Leu Gln Gly Ile Met Arg Leu Tyr Gln
    130                 135                 140
Thr Arg Leu Gln Ala Trp Leu Val Asn Lys Asn Asp Asp Asn Arg Arg
145                 150                 155                 160
Ala Leu Val Thr Gln Tyr Ala Ile Val Asp Asn Phe Phe Glu Lys Asn
                165                 170                 175
Met Pro Lys Phe Lys Glu Arg Asn Phe Glu Ile Leu Leu Leu Pro Val
            180                 185                 190
Tyr Ala Gln Ala Ala Asn Leu His Leu Ile Leu Leu Arg Asp Ala Asp
        195                 200                 205
Tyr Phe Gly Ala Gln Trp Gln Leu Gly Asp Asp Glu Ile Arg Asp Asn
    210                 215                 220
Tyr Ile Arg Leu Gln Gly Leu Ile Arg Glu Tyr Lys Asp His Cys Ile
225                 230                 235                 240
Thr Phe Tyr Asn Gln Gly Leu Asn Gln Phe Asn Arg Ser Asn Ala Gln
                245                 250                 255
Asp Trp Val Ser Phe Asn Arg Phe Arg Thr Asp Met Thr Leu Thr Val
            260                 265                 270
Leu Asp Leu Ala Ile Leu Phe Pro Asn Tyr Asp Pro Arg Arg Tyr Pro
        275                 280                 285
Leu Ala Val Lys Thr Glu Leu Thr Arg Glu Val Tyr Thr Asp Pro Val
    290                 295                 300
Gly Phe Thr Gly Val Leu Glu Ser Gly Gly Arg Thr Tyr Pro Trp Tyr
305                 310                 315                 320
Asn Pro Asn Asn Thr Thr Phe Thr Ala Met Glu Asn Asn Ala Arg Arg
                325                 330                 335
Arg Pro Ser Tyr Thr Thr Trp Leu Asn Arg Ile Phe Val Tyr Thr Arg
            340                 345                 350
Thr Leu Gly Asn Met Ser Asp Val Arg Asn Ile Trp Gly Gly His Thr
        355                 360                 365
Leu Val Glu Asn Gly Asn Asp Gly Ser Glu Ile Thr His Asn Phe Gly
    370                 375                 380
Lys Thr Asp Ser Ile Thr Pro Ile Gln Tyr Phe Asn Phe Ala Asn Leu
385                 390                 395                 400
Ser Val Phe Ser Ile Glu Ser Leu Ala Arg Ile Tyr Leu Gly Gly Thr
                405                 410                 415
Glu Ala Asn Asn Tyr Ile Thr Ser Gln Tyr Gly Val Ser Arg Val Ile
            420                 425                 430
Phe Asn Thr Ser Asn Ile Asn Asn Val Pro Gly Ser Leu Arg Tyr Glu
        435                 440                 445
Val Pro Ala Asn Leu Pro Ser Gln Thr Ile Leu Ser Glu Leu Pro Gly
    450                 455                 460
Lys Asp Lys Pro Arg Pro Asn Ala Gly Asp Phe Ser His Arg Leu Ser
465                 470                 475                 480
Tyr Ile Ser Asn Phe Asp Ala Arg Arg Ser Ser Ser Gly Gly Ile Val
                485                 490                 495
Ser Leu Leu Thr Phe Gly Trp Ala His Thr Ser Met Asp Arg Asn Asn
            500                 505                 510
Arg Leu Glu Pro Asp Lys Ile Thr Gln Ile Asp Ala Val Lys Gly Trp
        515                 520                 525
Gly Gly Asn Ile Gly Phe Val Ile Pro Gly Pro Thr Gly Gly Asn Leu
    530                 535                 540
Val Lys Val Ser Asp Ser Trp His Ser Leu Lys Val Gln Ala Pro Gln
545                 550                 555                 560
Arg Gln Thr Ser Tyr Arg Ile Arg Leu Arg Tyr Ala Cys Leu Val Thr
                565                 570                 575
His Gly Asp Ala Ile Phe Val Glu His Ser Gly Ser Ser His Ile Val
            580                 585                 590
Ser Phe Phe Asp Cys Ser Asn Ser Ser Gly Arg Pro Ser Asn Thr Leu
        595                 600                 605
Leu Glu Ser Asp Phe Arg Tyr Ile Asp Val Pro Gly Ile Phe Thr Pro
    610                 615                 620
Ser Ile Asn Pro Leu Ile Arg Tyr Arg Thr Gln Ser Phe Gly Thr His
625                 630                 635                 640
Ala Ile Asp Lys Phe Glu Phe Ile Pro Leu Asn Thr Phe Pro Asn Gln
                645                 650                 655
Ser Leu Glu Lys Arg Glu Gln Glu Val Asn Asp Leu Phe Ile Asn
            660                 665                 670
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<210> 23
<211> 1986
<212> DNA
<213> Bacillus thuringiensis

<220>
<221> CDS
<222> (1)...(1986)

<400> 23

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atg tct aat tgt tat cca agg tat cca cta gca aaa gat cca caa atg   48
Met Ser Asn Cys Tyr Pro Arg Tyr Pro Leu Ala Lys Asp Pro Gln Met
 1               5                  10                  15

act atg cga aac acg aac tat aaa gaa tgg cta aat atg tgt gat tca   96
Thr Met Arg Asn Thr Asn Tyr Lys Glu Trp Leu Asn Met Cys Asp Ser
            20                  25                  30

aat aca caa ttt att ggt gat ata agc acg tat tct agc cct gaa gct   144
Asn Thr Gln Phe Ile Gly Asp Ile Ser Thr Tyr Ser Ser Pro Glu Ala
        35                  40                  45

gct tta agt gta cga gat gct gtt tta acg ggt att aac agt gta ggg   192
Ala Leu Ser Val Arg Asp Ala Val Leu Thr Gly Ile Asn Ser Val Gly
    50                  55                  60

act ata ctt tcg aat tta ggg gtc cct ttg gca agt caa tca ttt gga   240
Thr Ile Leu Ser Asn Leu Gly Val Pro Leu Ala Ser Gln Ser Phe Gly
65                  70                  75                  80

ata att agt agg cta ata ggt att tta tgg gca ggg cct gat cca ttt   288
Ile Ile Ser Arg Leu Ile Gly Ile Leu Trp Ala Gly Pro Asp Pro Phe
                85                  90                  95

gaa gca ctt atg gtt ctt gtt gaa gag ctt att aag aaa agt ata gat   336
Glu Ala Leu Met Val Leu Val Glu Glu Leu Ile Lys Lys Ser Ile Asp
            100                 105                 110

cag cgt gta aga gaa aat gct ctt aga gag cta gaa ggt tta cag gga   384
Gln Arg Val Arg Glu Asn Ala Leu Arg Glu Leu Glu Gly Leu Gln Gly
        115                 120                 125

att atg aga cta tat caa act aga ctg caa gca tgg cta gtt aac aag   432
Ile Met Arg Leu Tyr Gln Thr Arg Leu Gln Ala Trp Leu Val Asn Lys
    130                 135                 140

aat gat gac aat cgg agg gca cta gta acg cag tat gca att gtt gat   480
Asn Asp Asp Asn Arg Arg Ala Leu Val Thr Gln Tyr Ala Ile Val Asp
145                 150                 155                 160

aac ttt ttc gaa aag aat atg cca aaa ttc aag gaa aga aac ttt gaa   528
Asn Phe Phe Glu Lys Asn Met Pro Lys Phe Lys Glu Arg Asn Phe Glu
                165                 170                 175

att tta ttg tta cca gta tat gca caa gcc gcg aat ttg cat tta att   576
Ile Leu Leu Leu Pro Val Tyr Ala Gln Ala Ala Asn Leu His Leu Ile
            180                 185                 190

tta tta aga gat gct gat tat ttt gga gca cag tgg caa tta ggt gat   624
Leu Leu Arg Asp Ala Asp Tyr Phe Gly Ala Gln Trp Gln Leu Gly Asp
        195                 200                 205

gat gaa att cgt gat aat tat atc aga cta caa gga ctg att aga gaa   672
Asp Glu Ile Arg Asp Asn Tyr Ile Arg Leu Gln Gly Leu Ile Arg Glu
    210                 215                 220
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```
tat aaa gat cat tgt ata aca ttc tat aac cag ggt tta aat caa ttt   720
Tyr Lys Asp His Cys Ile Thr Phe Tyr Asn Gln Gly Leu Asn Gln Phe
225                 230                 235                 240

aat cgc tca aat gct caa gat tgg gtg agc ttt aat agg ttt cgt aca   768
Asn Arg Ser Asn Ala Gln Asp Trp Val Ser Phe Asn Arg Phe Arg Thr
                245                 250                 255

gat atg aca tta aca gta tta gat ctc gca ata tta ttt cca aac tat   816
Asp Met Thr Leu Thr Val Leu Asp Leu Ala Ile Leu Phe Pro Asn Tyr
            260                 265                 270

gat cca cgt agg tat cca tta gca gta aaa acg gaa ttg act agg gaa   864
Asp Pro Arg Arg Tyr Pro Leu Ala Val Lys Thr Glu Leu Thr Arg Glu
        275                 280                 285

gtt tat aca gat cca gta ggg ttt act ggg gta tta gaa agt gga ggt   912
Val Tyr Thr Asp Pro Val Gly Phe Thr Gly Val Leu Glu Ser Gly Gly
    290                 295                 300

agg act tac cct tgg tat aat cct aat aat aca acc ttt act gct atg   960
Arg Thr Tyr Pro Trp Tyr Asn Pro Asn Asn Thr Thr Phe Thr Ala Met
305                 310                 315                 320

gaa aat aac gca aga cga cgt cct tct tat acc act tgg ctt aat cgt   1008
Glu Asn Asn Ala Arg Arg Arg Pro Ser Tyr Thr Thr Trp Leu Asn Arg
                325                 330                 335

att ttt gta tat aca agg act cta ggt aat atg tct gat gtg aga aat   1056
Ile Phe Val Tyr Thr Arg Thr Leu Gly Asn Met Ser Asp Val Arg Asn
            340                 345                 350

att tgg gga ggg cat aca tta gtt gaa aat gga aat gat ggt tct gaa   1104
Ile Trp Gly Gly His Thr Leu Val Glu Asn Gly Asn Asp Gly Ser Glu
        355                 360                 365

ata acc cat aac ttt ggt aaa act gat tct att act cct att caa tat   1152
Ile Thr His Asn Phe Gly Lys Thr Asp Ser Ile Thr Pro Ile Gln Tyr
    370                 375                 380

ttt aat ttc gcg aac ctt tct gtt ttc agt att gag tca ctt gct cgt   1200
Phe Asn Phe Ala Asn Leu Ser Val Phe Ser Ile Glu Ser Leu Ala Arg
385                 390                 395                 400

ata tat tta gga gga aca gag gct aat aat tat att act agt cag tat   1248
Ile Tyr Leu Gly Gly Thr Glu Ala Asn Asn Tyr Ile Thr Ser Gln Tyr
                405                 410                 415

gga gtc tcg aga gtt att ttt aat aca tca aat ata aat aat gta cct   1296
Gly Val Ser Arg Val Ile Phe Asn Thr Ser Asn Ile Asn Asn Val Pro
            420                 425                 430

gga tct tta aga tac gaa gtg cct gct aat ctt cca tcc caa act ata   1344
Gly Ser Leu Arg Tyr Glu Val Pro Ala Asn Leu Pro Ser Gln Thr Ile
        435                 440                 445

tta tca gaa tta cca gga aag gat aag cca aga cca aac gca gga gat   1392
Leu Ser Glu Leu Pro Gly Lys Asp Lys Pro Arg Pro Asn Ala Gly Asp
    450                 455                 460

ttc agc cat aga tta tct tat ata tca aat ttt gat gca cgg cga agt   1440
Phe Ser His Arg Leu Ser Tyr Ile Ser Asn Phe Asp Ala Arg Arg Ser
465                 470                 475                 480

agt tca ggc ggt att gtt agt ctt tta acg ttt ggt tgg gca cat acc   1488
Ser Ser Gly Gly Ile Val Ser Leu Leu Thr Phe Gly Trp Ala His Thr
                485                 490                 495
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agt atg gat cgt aat aat cgt ctt gaa cca gat aaa att act caa ata   1536
Ser Met Asp Arg Asn Asn Arg Leu Glu Pro Asp Lys Ile Thr Gln Ile
            500                 505                 510

gat gca gtt aaa ggt tgg ggg ggg aat atc ggg ttt gtc atc cca gga   1584
Asp Ala Val Lys Gly Trp Gly Gly Asn Ile Gly Phe Val Ile Pro Gly
        515                 520                 525

cct act ggg ggg aat ttg gta aaa gtc agt gat agt tgg cat tca ctt   1632
Pro Thr Gly Gly Asn Leu Val Lys Val Ser Asp Ser Trp His Ser Leu
    530                 535                 540

aaa gtt caa gca cca caa aga caa aca agt tat cgt att cgt ttg cgt   1680
Lys Val Gln Ala Pro Gln Arg Gln Thr Ser Tyr Arg Ile Arg Leu Arg
545                 550                 555                 560

tat gct tgt tta gtt acc cat ggg gat gct att ttt gta gaa cac agc   1728
Tyr Ala Cys Leu Val Thr His Gly Asp Ala Ile Phe Val Glu His Ser
                565                 570                 575

ggc agt agt cat ata gtt tca ttt ttt gat tgc tca aat tca tca ggt   1776
Gly Ser Ser His Ile Val Ser Phe Phe Asp Cys Ser Asn Ser Ser Gly
            580                 585                 590

cgt cca tca aac act ctt cta gag agt gat ttt cgc tat att gat gtt   1824
Arg Pro Ser Asn Thr Leu Leu Glu Ser Asp Phe Arg Tyr Ile Asp Val
        595                 600                 605

cca ggt att ttt aca cca tca ata aat ccc tta ata aga tat aga aca   1872
Pro Gly Ile Phe Thr Pro Ser Ile Asn Pro Leu Ile Arg Tyr Arg Thr
    610                 615                 620

caa agc ttt ggt acc cac gcg ata gac aaa ttt gaa ttt att cca ctt   1920
Gln Ser Phe Gly Thr His Ala Ile Asp Lys Phe Glu Phe Ile Pro Leu
625                 630                 635                 640

aac act ttt ccg aat caa tca tta gaa aaa aga gaa cag gaa gta aat   1968
Asn Thr Phe Pro Asn Gln Ser Leu Glu Lys Arg Glu Gln Glu Val Asn
                645                 650                 655

gat cta ttt atc aat taa                                         1986
Asp Leu Phe Ile Asn  *
            660
```

<210> 24
<211> 661
<212> PRT
<213> Bacillus thuringiensis

<400> 24

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Met Ser Asn Cys Tyr Pro Arg Tyr Pro Leu Ala Lys Asp Pro Gln Met
 1               5                  10                  15
Thr Met Arg Asn Thr Asn Tyr Lys Glu Trp Leu Asn Met Cys Asp Ser
            20                  25                  30
Asn Thr Gln Phe Ile Gly Asp Ile Ser Thr Tyr Ser Ser Pro Glu Ala
        35                  40                  45
Ala Leu Ser Val Arg Asp Ala Val Leu Thr Gly Ile Asn Ser Val Gly
    50                  55                  60
Thr Ile Leu Ser Asn Leu Gly Val Pro Leu Ala Ser Gln Ser Phe Gly
65                  70                  75                  80
Ile Ile Ser Arg Leu Ile Gly Ile Leu Trp Ala Gly Pro Asp Pro Phe
                85                  90                  95
Glu Ala Leu Met Val Leu Val Glu Glu Leu Ile Lys Lys Ser Ile Asp
            100                 105                 110
Gln Arg Val Arg Glu Asn Ala Leu Arg Glu Leu Glu Gly Leu Gln Gly
        115                 120                 125
Ile Met Arg Leu Tyr Gln Thr Arg Leu Gln Ala Trp Leu Val Asn Lys
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    130                 135                 140
Asn Asp Asp Asn Arg Arg Ala Leu Val Thr Gln Tyr Ala Ile Val Asp
145                 150                 155                 160
Asn Phe Phe Glu Lys Asn Met Pro Lys Phe Lys Glu Arg Asn Phe Glu
                165                 170                 175
Ile Leu Leu Leu Pro Val Tyr Ala Gln Ala Ala Asn Leu His Leu Ile
            180                 185                 190
Leu Leu Arg Asp Ala Asp Tyr Phe Gly Ala Gln Trp Gln Leu Gly Asp
        195                 200                 205
Asp Glu Ile Arg Asp Asn Tyr Ile Arg Leu Gln Gly Leu Ile Arg Glu
    210                 215                 220
Tyr Lys Asp His Cys Ile Thr Phe Tyr Asn Gln Gly Leu Asn Gln Phe
225                 230                 235                 240
Asn Arg Ser Asn Ala Gln Asp Trp Val Ser Phe Asn Arg Phe Arg Thr
                245                 250                 255
Asp Met Thr Leu Thr Val Leu Asp Leu Ala Ile Leu Phe Pro Asn Tyr
            260                 265                 270
Asp Pro Arg Arg Tyr Pro Leu Ala Val Lys Thr Glu Leu Thr Arg Glu
        275                 280                 285
Val Tyr Thr Asp Pro Val Gly Phe Thr Gly Val Leu Glu Ser Gly Gly
    290                 295                 300
Arg Thr Tyr Pro Trp Tyr Asn Pro Asn Asn Thr Thr Phe Thr Ala Met
305                 310                 315                 320
Glu Asn Asn Ala Arg Arg Arg Pro Ser Tyr Thr Thr Trp Leu Asn Arg
                325                 330                 335
Ile Phe Val Tyr Thr Arg Thr Leu Gly Asn Met Ser Asp Val Arg Asn
            340                 345                 350
Ile Trp Gly Gly His Thr Leu Val Glu Asn Gly Asn Asp Gly Ser Glu
        355                 360                 365
Ile Thr His Asn Phe Gly Lys Thr Asp Ser Ile Thr Pro Ile Gln Tyr
    370                 375                 380
Phe Asn Phe Ala Asn Leu Ser Val Phe Ser Ile Glu Ser Leu Ala Arg
385                 390                 395                 400
Ile Tyr Leu Gly Gly Thr Glu Ala Asn Asn Tyr Ile Thr Ser Gln Tyr
                405                 410                 415
Gly Val Ser Arg Val Ile Phe Asn Thr Ser Asn Ile Asn Asn Val Pro
            420                 425                 430
Gly Ser Leu Arg Tyr Glu Val Pro Ala Asn Leu Pro Ser Gln Thr Ile
        435                 440                 445
Leu Ser Glu Leu Pro Gly Lys Asp Lys Pro Arg Pro Asn Ala Gly Asp
    450                 455                 460
Phe Ser His Arg Leu Ser Tyr Ile Ser Asn Phe Asp Ala Arg Arg Ser
465                 470                 475                 480
Ser Ser Gly Gly Ile Val Ser Leu Leu Thr Phe Gly Trp Ala His Thr
                485                 490                 495
Ser Met Asp Arg Asn Asn Arg Leu Glu Pro Asp Lys Ile Thr Gln Ile
            500                 505                 510
Asp Ala Val Lys Gly Trp Gly Gly Asn Ile Gly Phe Val Ile Pro Gly
        515                 520                 525
Pro Thr Gly Gly Asn Leu Val Lys Val Ser Asp Ser Trp His Ser Leu
    530                 535                 540
Lys Val Gln Ala Pro Gln Arg Gln Thr Ser Tyr Arg Ile Arg Leu Arg
545                 550                 555                 560
Tyr Ala Cys Leu Val Thr His Gly Asp Ala Ile Phe Val Glu His Ser
                565                 570                 575
Gly Ser Ser His Ile Val Ser Phe Phe Asp Cys Ser Asn Ser Ser Gly
            580                 585                 590
Arg Pro Ser Asn Thr Leu Leu Glu Ser Asp Phe Arg Tyr Ile Asp Val
        595                 600                 605
Pro Gly Ile Phe Thr Pro Ser Ile Asn Pro Leu Ile Arg Tyr Arg Thr
    610                 615                 620
Gln Ser Phe Gly Thr His Ala Ile Asp Lys Phe Glu Phe Ile Pro Leu
625                 630                 635                 640
Asn Thr Phe Pro Asn Gln Ser Leu Glu Lys Arg Glu Gln Glu Val Asn
                645                 650                 655
Asp Leu Phe Ile Asn
            660
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<210> 25
<211> 2145
<212> DNA
<213> Bacillus thuringiensis

<400> 25
tttcaccaaa tataatgttt ttttgtagaa acattgttac aggaatacat tggggtacta 60
cgaatatata gaaagacacc tggcatatat ttattaggtg tcttaaaaat aaggactata 120
taaggagtga aaaatatgaa ttcttatcaa aatacaaatg aatatgaaat tctggatggt 180
tccccgaata acacaaatat gtcaaacaga tatccttttg caaaggatcc aaatatattt 240
cctattaacc tggacgcttg tcagggaagg ccatggcaag atacgtggga atcagtctcg 300
gatatagtaa ctattgggac ataccttata caattcttgc tagaacccgg tataggtgga 360
attcctgtaa tattttcaat aataaacaaa ctcattccgt cttctggtca atctgtggca 420
gcactttcta tatgtgattt agtatctata attcgtaaag aggtagacga gagcgtgtta 480
agtgacgggg ttgcagattt tgagggtgaa atgactgctt atcaagatta ttatcttcat 540
tatcttgagg attggcttac agataaatca aatcctaaaa aacttgctga cgtagttaaa 600
cagttccaag cacgggaaga agatttcact aaacttttag cagggtcatt atcaagacag 660
aaagctgaaa tattattatt gcctacgtat gtgcaagctg caaatgtgca tttattacta 720
ttaagggacg cagttaaata taaaaaagaa tggggactag tgtgtccacc gttgtatcca 780
gggtcaggga gaactgattg taacgagcgg ttaaaagcga aaataaaaga gtatactaat 840
tattgtgtag ggtggtataa caagggttta gatcagataa gacaggcggg tacaagtgct 900
gaagtttggt cgaaatttaa taaatttcgt agagaaatga cgttggcggt attggatatt 960
attgctatat ttccaactta tgattttgaa aaatatccat tagcaacaag tgtagagtta 1020
actagggaaa tttatacaga tccagtggga tattcagggg gaaattatgg ttgggaacgg 1080
ttttttagct ttaattcggt agaagcaaat ggaacacggg gacctggttt agttacttgg 1140
cttcaagcta tagatatata tagtcattct attaatcttc agcttggtta tcttagtggc 1200
tgggggggaa ctcgtcatta tgaagacttc acaaagggta acggtgcttt tcaacgtatg 1260
tctggaacta cgagtaataa tccacgtaat attatttttg gcaataccga tatatttaaa 1320
attatttcat tagctagata tgcaatgcaa ccgtttgttg ggtattcaat cccacggcat 1380
cttgtttcac gtgcagaatt ttttccgaca acactaaata ctttcctgta tgaggtaaac 1440
agttctgggt actcacagac aattgaatct gtgttaccag gtattaataa ggatctacca 1500
cctagtcgta caaattactc tcatagatta tcaaatgcgg catgtgttca aaatgaaacc 1560
tccagagtta acgtatttgg ttggacacat acaagtatga aaaaagataa tcgaatttat 1620
ccagataaaa ttacgcaaat tcctgcagta aaagcttttg ccctaccagc aggtacagga 1680
tatgcaggag gttacgtcac agctgggcct ggttatacag gaggagatgt agtaacgtta 1740
ccttatcaag caagtttaaa aatacgttta acttctgcac ccacgaataa aaattaccgt 1800
gttagacttc gctacgcgag tggaggacct ggtccgttcc gagtagaaag atggtcgcca 1860
agttctgttt caaatgctaa tttttctcgt ccagctacag gtggctatag ttcatttgat 1920
tatgtggaca ccttagttac tacatttaat caatcaggtg ttgaaataat tatacaaaat 1980
ctatctggtt accaccttat tgttgacaaa gtcgaattta tcccaattga catccaaatt 2040
gaaaaatgta cgaaatgtca attcgaagga gacatatgta gatgtgaagg agtacaatcc 2100
ttggaaacaa aaaaagagat tgtaaatagt ttatttatca attaa 2145

<210> 26
<211> 2019
<212> DNA
<213> Bacillus thuringiensis

<220>
<221> CDS
<222> (1)...(2019)

<400> 26
gtg aaa aat atg aat tct tat caa aat aca aat gaa tat gaa att ctg 48
Met Lys Asn Met Asn Ser Tyr Gln Asn Thr Asn Glu Tyr Glu Ile Leu
1 5 10 15

gat ggt tcc ccg aat aac aca aat atg tca aac aga tat cct ttt gca 96
Asp Gly Ser Pro Asn Asn Thr Asn Met Ser Asn Arg Tyr Pro Phe Ala
20 25 30

aag gat cca aat ata ttt cct att aac ctg gac gct tgt cag gga agg 144
Lys Asp Pro Asn Ile Phe Pro Ile Asn Leu Asp Ala Cys Gln Gly Arg
35 40 45

cca tgg caa gat acg tgg gaa tca gtc tcg gat ata gta act att ggg 192
Pro Trp Gln Asp Thr Trp Glu Ser Val Ser Asp Ile Val Thr Ile Gly

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     50                  55                  60

aca tac ctt ata caa ttc ttg cta gaa ccc ggt ata ggt gga att cct   240
Thr Tyr Leu Ile Gln Phe Leu Leu Glu Pro Gly Ile Gly Gly Ile Pro
 65                  70                  75                  80

gta ata ttt tca ata ata aac aaa ctc att ccg tct tct ggt caa tct   288
Val Ile Phe Ser Ile Ile Asn Lys Leu Ile Pro Ser Ser Gly Gln Ser
                85                  90                  95

gtg gca gca ctt tct ata tgt gat tta gta tct ata att cgt aaa gag   336
Val Ala Ala Leu Ser Ile Cys Asp Leu Val Ser Ile Ile Arg Lys Glu
            100                 105                 110

gta gac gag agc gtg tta agt gac ggg gtt gca gat ttt gag ggt gaa   384
Val Asp Glu Ser Val Leu Ser Asp Gly Val Ala Asp Phe Glu Gly Glu
        115                 120                 125

atg act gct tat caa gat tat tat ctt cat tat ctt gag gat tgg ctt   432
Met Thr Ala Tyr Gln Asp Tyr Tyr Leu His Tyr Leu Glu Asp Trp Leu
    130                 135                 140

aca gat aaa tca aat cct aaa aaa ctt gct gac gta gtt aaa cag ttc   480
Thr Asp Lys Ser Asn Pro Lys Lys Leu Ala Asp Val Val Lys Gln Phe
145                 150                 155                 160

caa gca cgg gaa gaa gat ttc act aaa ctt tta gca ggg tca tta tca   528
Gln Ala Arg Glu Glu Asp Phe Thr Lys Leu Leu Ala Gly Ser Leu Ser
                165                 170                 175

aga cag aaa gct gaa ata tta tta ttg cct acg tat gtg caa gct gca   576
Arg Gln Lys Ala Glu Ile Leu Leu Leu Pro Thr Tyr Val Gln Ala Ala
            180                 185                 190

aat gtg cat tta tta cta tta agg gac gca gtt aaa tat aaa aaa gaa   624
Asn Val His Leu Leu Leu Leu Arg Asp Ala Val Lys Tyr Lys Lys Glu
        195                 200                 205

tgg gga cta gtg tgt cca ccg ttg tat cca ggg tca ggg aga act gat   672
Trp Gly Leu Val Cys Pro Pro Leu Tyr Pro Gly Ser Gly Arg Thr Asp
    210                 215                 220

tgt aac gag cgg tta aaa gcg aaa ata aaa gag tat act aat tat tgt   720
Cys Asn Glu Arg Leu Lys Ala Lys Ile Lys Glu Tyr Thr Asn Tyr Cys
225                 230                 235                 240

gta ggg tgg tat aac aag ggt tta gat cag ata aga cag gcg ggt aca   768
Val Gly Trp Tyr Asn Lys Gly Leu Asp Gln Ile Arg Gln Ala Gly Thr
                245                 250                 255

agt gct gaa gtt tgg tcg aaa ttt aat aaa ttt cgt aga gaa atg acg   816
Ser Ala Glu Val Trp Ser Lys Phe Asn Lys Phe Arg Arg Glu Met Thr
            260                 265                 270

ttg gcg gta ttg gat att att gct ata ttt cca act tat gat ttt gaa   864
Leu Ala Val Leu Asp Ile Ile Ala Ile Phe Pro Thr Tyr Asp Phe Glu
        275                 280                 285

aaa tat cca tta gca aca agt gta gag tta act agg gaa att tat aca   912
Lys Tyr Pro Leu Ala Thr Ser Val Glu Leu Thr Arg Glu Ile Tyr Thr
    290                 295                 300

gat cca gtg gga tat tca ggg gga aat tat ggt tgg gaa cgg ttt ttt   960
Asp Pro Val Gly Tyr Ser Gly Gly Asn Tyr Gly Trp Glu Arg Phe Phe
305                 310                 315                 320

agc ttt aat tcg gta gaa gca aat gga aca cgg gga cct ggt tta gtt   1008
Ser Phe Asn Ser Val Glu Ala Asn Gly Thr Arg Gly Pro Gly Leu Val
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                325                 330                 335

act tgg ctt caa gct ata gat ata tat agt cat tct att aat ctt cag   1056
Thr Trp Leu Gln Ala Ile Asp Ile Tyr Ser His Ser Ile Asn Leu Gln
            340                 345                 350

ctt ggt tat ctt agt ggc tgg ggg gga act cgt cat tat gaa gac ttc   1104
Leu Gly Tyr Leu Ser Gly Trp Gly Gly Thr Arg His Tyr Glu Asp Phe
        355                 360                 365

aca aag ggt aac ggt gct ttt caa cgt atg tct gga act acg agt aat   1152
Thr Lys Gly Asn Gly Ala Phe Gln Arg Met Ser Gly Thr Thr Ser Asn
    370                 375                 380

aat cca cgt aat att att ttt ggc aat acc gat ata ttt aaa att att   1200
Asn Pro Arg Asn Ile Ile Phe Gly Asn Thr Asp Ile Phe Lys Ile Ile
385                 390                 395                 400

tca tta gct aga tat gca atg caa ccg ttt gtt ggg tat tca atc cca   1248
Ser Leu Ala Arg Tyr Ala Met Gln Pro Phe Val Gly Tyr Ser Ile Pro
                405                 410                 415

cgg cat ctt gtt tca cgt gca gaa ttt ttt ccg aca aca cta aat act   1296
Arg His Leu Val Ser Arg Ala Glu Phe Phe Pro Thr Thr Leu Asn Thr
            420                 425                 430

ttc ctg tat gag gta aac agt tct ggg tac tca cag aca att gaa tct   1344
Phe Leu Tyr Glu Val Asn Ser Ser Gly Tyr Ser Gln Thr Ile Glu Ser
        435                 440                 445

gtg tta cca ggt att aat aag gat cta cca cct agt cgt aca aat tac   1392
Val Leu Pro Gly Ile Asn Lys Asp Leu Pro Pro Ser Arg Thr Asn Tyr
    450                 455                 460

tct cat aga tta tca aat gcg gca tgt gtt caa aat gaa acc tcc aga   1440
Ser His Arg Leu Ser Asn Ala Ala Cys Val Gln Asn Glu Thr Ser Arg
465                 470                 475                 480

gtt aac gta ttt ggt tgg aca cat aca agt atg aaa aaa gat aat cga   1488
Val Asn Val Phe Gly Trp Thr His Thr Ser Met Lys Lys Asp Asn Arg
                485                 490                 495

att tat cca gat aaa att acg caa att cct gca gta aaa gct ttt gcc   1536
Ile Tyr Pro Asp Lys Ile Thr Gln Ile Pro Ala Val Lys Ala Phe Ala
            500                 505                 510

cta cca gca ggt aca gga tat gca gga ggt tac gtc aca gct ggg cct   1584
Leu Pro Ala Gly Thr Gly Tyr Ala Gly Gly Tyr Val Thr Ala Gly Pro
        515                 520                 525

ggt tat aca gga gga gat gta gta acg tta cct tat caa gca agt tta   1632
Gly Tyr Thr Gly Gly Asp Val Val Thr Leu Pro Tyr Gln Ala Ser Leu
    530                 535                 540

aaa ata cgt tta act tct gca ccc acg aat aaa aat tac cgt gtt aga   1680
Lys Ile Arg Leu Thr Ser Ala Pro Thr Asn Lys Asn Tyr Arg Val Arg
545                 550                 555                 560

ctt cgc tac gcg agt gga gga cct ggt ccg ttc cga gta gaa aga tgg   1728
Leu Arg Tyr Ala Ser Gly Gly Pro Gly Pro Phe Arg Val Glu Arg Trp
                565                 570                 575

tcg cca agt tct gtt tca aat gct aat ttt tct cgt cca gct aca ggt   1776
Ser Pro Ser Ser Val Ser Asn Ala Asn Phe Ser Arg Pro Ala Thr Gly
            580                 585                 590

ggc tat agt tca ttt gat tat gtg gac acc tta gtt act aca ttt aat   1824
Gly Tyr Ser Ser Phe Asp Tyr Val Asp Thr Leu Val Thr Thr Phe Asn
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        595                 600                 605

caa tca ggt gtt gaa ata att ata caa aat cta tct ggt tac cac ctt   1872
Gln Ser Gly Val Glu Ile Ile Ile Gln Asn Leu Ser Gly Tyr His Leu
    610                 615                 620

att gtt gac aaa gtc gaa ttt atc cca att gac atc caa att gaa aaa   1920
Ile Val Asp Lys Val Glu Phe Ile Pro Ile Asp Ile Gln Ile Glu Lys
625                 630                 635                 640

tgt acg aaa tgt caa ttc gaa gga gac ata tgt aga tgt gaa gga gta   1968
Cys Thr Lys Cys Gln Phe Glu Gly Asp Ile Cys Arg Cys Glu Gly Val
                645                 650                 655

caa tcc ttg gaa aca aaa aaa gag att gta aat agt tta ttt atc aat   2016
Gln Ser Leu Glu Thr Lys Lys Glu Ile Val Asn Ser Leu Phe Ile Asn
            660                 665                 670

taa                                                              2019
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<210> 27
<211> 672
<212> PRT
<213> Bacillus thuringiensis

<400> 27

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Met Lys Asn Met Asn Ser Tyr Gln Asn Thr Asn Glu Tyr Glu Ile Leu
 1               5                  10                  15
Asp Gly Ser Pro Asn Asn Thr Asn Met Ser Asn Arg Tyr Pro Phe Ala
            20                  25                  30
Lys Asp Pro Asn Ile Phe Pro Ile Asn Leu Asp Ala Cys Gln Gly Arg
        35                  40                  45
Pro Trp Gln Asp Thr Trp Glu Ser Val Ser Asp Ile Val Thr Ile Gly
    50                  55                  60
Thr Tyr Leu Ile Gln Phe Leu Leu Glu Pro Gly Ile Gly Gly Ile Pro
65                  70                  75                  80
Val Ile Phe Ser Ile Ile Asn Lys Leu Ile Pro Ser Ser Gly Gln Ser
                85                  90                  95
Val Ala Ala Leu Ser Ile Cys Asp Leu Val Ser Ile Ile Arg Lys Glu
            100                 105                 110
Val Asp Glu Ser Val Leu Ser Asp Gly Val Ala Asp Phe Glu Gly Glu
        115                 120                 125
Met Thr Ala Tyr Gln Asp Tyr Tyr Leu His Tyr Leu Glu Asp Trp Leu
    130                 135                 140
Thr Asp Lys Ser Asn Pro Lys Lys Leu Ala Asp Val Val Lys Gln Phe
145                 150                 155                 160
Gln Ala Arg Glu Glu Asp Phe Thr Lys Leu Leu Ala Gly Ser Leu Ser
                165                 170                 175
Arg Gln Lys Ala Glu Ile Leu Leu Leu Pro Thr Tyr Val Gln Ala Ala
            180                 185                 190
Asn Val His Leu Leu Leu Leu Arg Asp Ala Val Lys Tyr Lys Lys Glu
        195                 200                 205
Trp Gly Leu Val Cys Pro Pro Leu Tyr Pro Gly Ser Gly Arg Thr Asp
    210                 215                 220
Cys Asn Glu Arg Leu Lys Ala Lys Ile Lys Glu Tyr Thr Asn Tyr Cys
225                 230                 235                 240
Val Gly Trp Tyr Asn Lys Gly Leu Asp Gln Ile Arg Gln Ala Gly Thr
                245                 250                 255
Ser Ala Glu Val Trp Ser Lys Phe Asn Lys Phe Arg Arg Glu Met Thr
            260                 265                 270
Leu Ala Val Leu Asp Ile Ile Ala Ile Phe Pro Thr Tyr Asp Phe Glu
        275                 280                 285
Lys Tyr Pro Leu Ala Thr Ser Val Glu Leu Thr Arg Glu Ile Tyr Thr
    290                 295                 300
Asp Pro Val Gly Tyr Ser Gly Gly Asn Tyr Gly Trp Glu Arg Phe Phe
```

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305                 310                 315                 320
Ser Phe Asn Ser Val Glu Ala Asn Gly Thr Arg Gly Pro Gly Leu Val
                325                 330                 335
Thr Trp Leu Gln Ala Ile Asp Ile Tyr Ser His Ser Ile Asn Leu Gln
            340                 345                 350
Leu Gly Tyr Leu Ser Gly Trp Gly Gly Thr Arg His Tyr Glu Asp Phe
        355                 360                 365
Thr Lys Gly Asn Gly Ala Phe Gln Arg Met Ser Gly Thr Thr Ser Asn
    370                 375                 380
Asn Pro Arg Asn Ile Ile Phe Gly Asn Thr Asp Ile Phe Lys Ile Ile
385                 390                 395                 400
Ser Leu Ala Arg Tyr Ala Met Gln Pro Phe Val Gly Tyr Ser Ile Pro
                405                 410                 415
Arg His Leu Val Ser Arg Ala Glu Phe Phe Pro Thr Thr Leu Asn Thr
            420                 425                 430
Phe Leu Tyr Glu Val Asn Ser Ser Gly Tyr Ser Gln Thr Ile Glu Ser
        435                 440                 445
Val Leu Pro Gly Ile Asn Lys Asp Leu Pro Pro Ser Arg Thr Asn Tyr
    450                 455                 460
Ser His Arg Leu Ser Asn Ala Ala Cys Val Gln Asn Glu Thr Ser Arg
465                 470                 475                 480
Val Asn Val Phe Gly Trp Thr His Thr Ser Met Lys Lys Asp Asn Arg
                485                 490                 495
Ile Tyr Pro Asp Lys Ile Thr Gln Ile Pro Ala Val Lys Ala Phe Ala
            500                 505                 510
Leu Pro Ala Gly Thr Gly Tyr Ala Gly Gly Tyr Val Thr Ala Gly Pro
        515                 520                 525
Gly Tyr Thr Gly Gly Asp Val Val Thr Leu Pro Tyr Gln Ala Ser Leu
    530                 535                 540
Lys Ile Arg Leu Thr Ser Ala Pro Thr Asn Lys Asn Tyr Arg Val Arg
545                 550                 555                 560
Leu Arg Tyr Ala Ser Gly Gly Pro Gly Pro Phe Arg Val Glu Arg Trp
                565                 570                 575
Ser Pro Ser Ser Val Ser Asn Ala Asn Phe Ser Arg Pro Ala Thr Gly
            580                 585                 590
Gly Tyr Ser Ser Phe Asp Tyr Val Asp Thr Leu Val Thr Thr Phe Asn
        595                 600                 605
Gln Ser Gly Val Glu Ile Ile Ile Gln Asn Leu Ser Gly Tyr His Leu
    610                 615                 620
Ile Val Asp Lys Val Glu Phe Ile Pro Ile Asp Ile Gln Ile Glu Lys
625                 630                 635                 640
Cys Thr Lys Cys Gln Phe Glu Gly Asp Ile Cys Arg Cys Glu Gly Val
                645                 650                 655
Gln Ser Leu Glu Thr Lys Lys Glu Ile Val Asn Ser Leu Phe Ile Asn
            660                 665                 670
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<210> 28
<211> 2010
<212> DNA
<213> Bacillus thuringiensis

<220>
<221> CDS
<222> (1)...(2010)

<400> 28

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atg aat tct tat caa aat aca aat gaa tat gaa att ctg gat ggt tcc   48
Met Asn Ser Tyr Gln Asn Thr Asn Glu Tyr Glu Ile Leu Asp Gly Ser
 1               5                  10                  15

ccg aat aac aca aat atg tca aac aga tat cct ttt gca aag gat cca   96
Pro Asn Asn Thr Asn Met Ser Asn Arg Tyr Pro Phe Ala Lys Asp Pro
             20                  25                  30

aat ata ttt cct att aac ctg gac gct tgt cag gga agg cca tgg caa   144
Asn Ile Phe Pro Ile Asn Leu Asp Ala Cys Gln Gly Arg Pro Trp Gln
         35                  40                  45
```

```
gat acg tgg gaa tca gtc tcg gat ata gta act att ggg aca tac ctt   192
Asp Thr Trp Glu Ser Val Ser Asp Ile Val Thr Ile Gly Thr Tyr Leu
     50                  55                  60

ata caa ttc ttg cta gaa ccc ggt ata ggt gga att cct gta ata ttt   240
Ile Gln Phe Leu Leu Glu Pro Gly Ile Gly Gly Ile Pro Val Ile Phe
 65                  70                  75                  80

tca ata ata aac aaa ctc att ccg tct tct ggt caa tct gtg gca gca   288
Ser Ile Ile Asn Lys Leu Ile Pro Ser Ser Gly Gln Ser Val Ala Ala
                 85                  90                  95

ctt tct ata tgt gat tta gta tct ata att cgt aaa gag gta gac gag   336
Leu Ser Ile Cys Asp Leu Val Ser Ile Ile Arg Lys Glu Val Asp Glu
            100                 105                 110

agc gtg tta agt gac ggg gtt gca gat ttt gag ggt gaa atg act gct   384
Ser Val Leu Ser Asp Gly Val Ala Asp Phe Glu Gly Glu Met Thr Ala
        115                 120                 125

tat caa gat tat tat ctt cat tat ctt gag gat tgg ctt aca gat aaa   432
Tyr Gln Asp Tyr Tyr Leu His Tyr Leu Glu Asp Trp Leu Thr Asp Lys
    130                 135                 140

tca aat cct aaa aaa ctt gct gac gta gtt aaa cag ttc caa gca cgg   480
Ser Asn Pro Lys Lys Leu Ala Asp Val Val Lys Gln Phe Gln Ala Arg
145                 150                 155                 160

gaa gaa gat ttc act aaa ctt tta gca ggg tca tta tca aga cag aaa   528
Glu Glu Asp Phe Thr Lys Leu Leu Ala Gly Ser Leu Ser Arg Gln Lys
                165                 170                 175

gct gaa ata tta tta ttg cct acg tat gtg caa gct gca aat gtg cat   576
Ala Glu Ile Leu Leu Leu Pro Thr Tyr Val Gln Ala Ala Asn Val His
            180                 185                 190

tta tta cta tta agg gac gca gtt aaa tat aaa aaa gaa tgg gga cta   624
Leu Leu Leu Leu Arg Asp Ala Val Lys Tyr Lys Lys Glu Trp Gly Leu
        195                 200                 205

gtg tgt cca ccg ttg tat cca ggg tca ggg aga act gat tgt aac gag   672
Val Cys Pro Pro Leu Tyr Pro Gly Ser Gly Arg Thr Asp Cys Asn Glu
    210                 215                 220

cgg tta aaa gcg aaa ata aaa gag tat act aat tat tgt gta ggg tgg   720
Arg Leu Lys Ala Lys Ile Lys Glu Tyr Thr Asn Tyr Cys Val Gly Trp
225                 230                 235                 240

tat aac aag ggt tta gat cag ata aga cag gcg ggt aca agt gct gaa   768
Tyr Asn Lys Gly Leu Asp Gln Ile Arg Gln Ala Gly Thr Ser Ala Glu
                245                 250                 255

gtt tgg tcg aaa ttt aat aaa ttt cgt aga gaa atg acg ttg gcg gta   816
Val Trp Ser Lys Phe Asn Lys Phe Arg Arg Glu Met Thr Leu Ala Val
            260                 265                 270

ttg gat att att gct ata ttt cca act tat gat ttt gaa aaa tat cca   864
Leu Asp Ile Ile Ala Ile Phe Pro Thr Tyr Asp Phe Glu Lys Tyr Pro
        275                 280                 285

tta gca aca agt gta gag tta act agg gaa att tat aca gat cca gtg   912
Leu Ala Thr Ser Val Glu Leu Thr Arg Glu Ile Tyr Thr Asp Pro Val
    290                 295                 300

gga tat tca ggg gga aat tat ggt tgg gaa cgg ttt ttt agc ttt aat   960
Gly Tyr Ser Gly Gly Asn Tyr Gly Trp Glu Arg Phe Phe Ser Phe Asn
305                 310                 315                 320
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tcg gta gaa gca aat gga aca cgg gga cct ggt tta gtt act tgg ctt   1008
Ser Val Glu Ala Asn Gly Thr Arg Gly Pro Gly Leu Val Thr Trp Leu
                325                 330                 335

caa gct ata gat ata tat agt cat tct att aat ctt cag ctt ggt tat   1056
Gln Ala Ile Asp Ile Tyr Ser His Ser Ile Asn Leu Gln Leu Gly Tyr
            340                 345                 350

ctt agt ggc tgg ggg gga act cgt cat tat gaa gac ttc aca aag ggt   1104
Leu Ser Gly Trp Gly Gly Thr Arg His Tyr Glu Asp Phe Thr Lys Gly
        355                 360                 365

aac ggt gct ttt caa cgt atg tct gga act acg agt aat aat cca cgt   1152
Asn Gly Ala Phe Gln Arg Met Ser Gly Thr Thr Ser Asn Asn Pro Arg
    370                 375                 380

aat att att ttt ggc aat acc gat ata ttt aaa att att tca tta gct   1200
Asn Ile Ile Phe Gly Asn Thr Asp Ile Phe Lys Ile Ile Ser Leu Ala
385                 390                 395                 400

aga tat gca atg caa ccg ttt gtt ggg tat tca atc cca cgg cat ctt   1248
Arg Tyr Ala Met Gln Pro Phe Val Gly Tyr Ser Ile Pro Arg His Leu
                405                 410                 415

gtt tca cgt gca gaa ttt ttt ccg aca aca cta aat act ttc ctg tat   1296
Val Ser Arg Ala Glu Phe Phe Pro Thr Thr Leu Asn Thr Phe Leu Tyr
            420                 425                 430

gag gta aac agt tct ggg tac tca cag aca att gaa tct gtg tta cca   1344
Glu Val Asn Ser Ser Gly Tyr Ser Gln Thr Ile Glu Ser Val Leu Pro
        435                 440                 445

ggt att aat aag gat cta cca cct agt cgt aca aat tac tct cat aga   1392
Gly Ile Asn Lys Asp Leu Pro Pro Ser Arg Thr Asn Tyr Ser His Arg
    450                 455                 460

tta tca aat gcg gca tgt gtt caa aat gaa acc tcc aga gtt aac gta   1440
Leu Ser Asn Ala Ala Cys Val Gln Asn Glu Thr Ser Arg Val Asn Val
465                 470                 475                 480

ttt ggt tgg aca cat aca agt atg aaa aaa gat aat cga att tat cca   1488
Phe Gly Trp Thr His Thr Ser Met Lys Lys Asp Asn Arg Ile Tyr Pro
                485                 490                 495

gat aaa att acg caa att cct gca gta aaa gct ttt gcc cta cca gca   1536
Asp Lys Ile Thr Gln Ile Pro Ala Val Lys Ala Phe Ala Leu Pro Ala
            500                 505                 510

ggt aca gga tat gca gga ggt tac gtc aca gct ggg cct ggt tat aca   1584
Gly Thr Gly Tyr Ala Gly Gly Tyr Val Thr Ala Gly Pro Gly Tyr Thr
        515                 520                 525

gga gga gat gta gta acg tta cct tat caa gca agt tta aaa ata cgt   1632
Gly Gly Asp Val Val Thr Leu Pro Tyr Gln Ala Ser Leu Lys Ile Arg
    530                 535                 540

tta act tct gca ccc acg aat aaa aat tac cgt gtt aga ctt cgc tac   1680
Leu Thr Ser Ala Pro Thr Asn Lys Asn Tyr Arg Val Arg Leu Arg Tyr
545                 550                 555                 560

gcg agt gga gga cct ggt ccg ttc cga gta gaa aga tgg tcg cca agt   1728
Ala Ser Gly Gly Pro Gly Pro Phe Arg Val Glu Arg Trp Ser Pro Ser
                565                 570                 575

tct gtt tca aat gct aat ttt tct cgt cca gct aca ggt ggc tat agt   1776
Ser Val Ser Asn Ala Asn Phe Ser Arg Pro Ala Thr Gly Gly Tyr Ser
            580                 585                 590
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```
tca ttt gat tat gtg gac acc tta gtt act aca ttt aat caa tca ggt   1824
Ser Phe Asp Tyr Val Asp Thr Leu Val Thr Thr Phe Asn Gln Ser Gly
        595                 600                 605

gtt gaa ata att ata caa aat cta tct ggt tac cac ctt att gtt gac   1872
Val Glu Ile Ile Ile Gln Asn Leu Ser Gly Tyr His Leu Ile Val Asp
    610                 615                 620

aaa gtc gaa ttt atc cca att gac atc caa att gaa aaa tgt acg aaa   1920
Lys Val Glu Phe Ile Pro Ile Asp Ile Gln Ile Glu Lys Cys Thr Lys
625                 630                 635                 640

tgt caa ttc gaa gga gac ata tgt aga tgt gaa gga gta caa tcc ttg   1968
Cys Gln Phe Glu Gly Asp Ile Cys Arg Cys Glu Gly Val Gln Ser Leu
                645                 650                 655

gaa aca aaa aaa gag att gta aat agt tta ttt atc aat taa           2010
Glu Thr Lys Lys Glu Ile Val Asn Ser Leu Phe Ile Asn  *
            660                 665
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<210> 29
<211> 669
<212> PRT
<213> Bacillus thuringiensis

<400> 29

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Met Asn Ser Tyr Gln Asn Thr Asn Glu Tyr Glu Ile Leu Asp Gly Ser
 1               5                  10                  15
Pro Asn Asn Thr Asn Met Ser Asn Arg Tyr Pro Phe Ala Lys Asp Pro
            20                  25                  30
Asn Ile Phe Pro Ile Asn Leu Asp Ala Cys Gln Gly Arg Pro Trp Gln
        35                  40                  45
Asp Thr Trp Glu Ser Val Ser Asp Ile Val Thr Ile Gly Thr Tyr Leu
    50                  55                  60
Ile Gln Phe Leu Leu Glu Pro Gly Ile Gly Gly Ile Pro Val Ile Phe
65                  70                  75                  80
Ser Ile Ile Asn Lys Leu Ile Pro Ser Ser Gly Gln Ser Val Ala Ala
                85                  90                  95
Leu Ser Ile Cys Asp Leu Val Ser Ile Ile Arg Lys Glu Val Asp Glu
            100                 105                 110
Ser Val Leu Ser Asp Gly Val Ala Asp Phe Glu Gly Glu Met Thr Ala
        115                 120                 125
Tyr Gln Asp Tyr Tyr Leu His Tyr Leu Glu Asp Trp Leu Thr Asp Lys
    130                 135                 140
Ser Asn Pro Lys Lys Leu Ala Asp Val Val Lys Gln Phe Gln Ala Arg
145                 150                 155                 160
Glu Glu Asp Phe Thr Lys Leu Leu Ala Gly Ser Leu Ser Arg Gln Lys
                165                 170                 175
Ala Glu Ile Leu Leu Leu Pro Thr Tyr Val Gln Ala Ala Asn Val His
            180                 185                 190
Leu Leu Leu Leu Arg Asp Ala Val Lys Tyr Lys Lys Glu Trp Gly Leu
        195                 200                 205
Val Cys Pro Pro Leu Tyr Pro Gly Ser Gly Arg Thr Asp Cys Asn Glu
    210                 215                 220
Arg Leu Lys Ala Lys Ile Lys Glu Tyr Thr Asn Tyr Cys Val Gly Trp
225                 230                 235                 240
Tyr Asn Lys Gly Leu Asp Gln Ile Arg Gln Ala Gly Thr Ser Ala Glu
                245                 250                 255
Val Trp Ser Lys Phe Asn Lys Phe Arg Arg Glu Met Thr Leu Ala Val
            260                 265                 270
Leu Asp Ile Ile Ala Ile Phe Pro Thr Tyr Asp Phe Glu Lys Tyr Pro
        275                 280                 285
Leu Ala Thr Ser Val Glu Leu Thr Arg Glu Ile Tyr Thr Asp Pro Val
    290                 295                 300
Gly Tyr Ser Gly Gly Asn Tyr Gly Trp Glu Arg Phe Phe Ser Phe Asn
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305                 310                 315                 320
Ser Val Glu Ala Asn Gly Thr Arg Gly Pro Gly Leu Val Thr Trp Leu
                325                 330                 335
Gln Ala Ile Asp Ile Tyr Ser His Ser Ile Asn Leu Gln Leu Gly Tyr
            340                 345                 350
Leu Ser Gly Trp Gly Gly Thr Arg His Tyr Glu Asp Phe Thr Lys Gly
        355                 360                 365
Asn Gly Ala Phe Gln Arg Met Ser Gly Thr Thr Ser Asn Asn Pro Arg
    370                 375                 380
Asn Ile Ile Phe Gly Asn Thr Asp Ile Phe Lys Ile Ile Ser Leu Ala
385                 390                 395                 400
Arg Tyr Ala Met Gln Pro Phe Val Gly Tyr Ser Ile Pro Arg His Leu
                405                 410                 415
Val Ser Arg Ala Glu Phe Phe Pro Thr Thr Leu Asn Thr Phe Leu Tyr
            420                 425                 430
Glu Val Asn Ser Ser Gly Tyr Ser Gln Thr Ile Glu Ser Val Leu Pro
        435                 440                 445
Gly Ile Asn Lys Asp Leu Pro Pro Ser Arg Thr Asn Tyr Ser His Arg
    450                 455                 460
Leu Ser Asn Ala Ala Cys Val Gln Asn Glu Thr Ser Arg Val Asn Val
465                 470                 475                 480
Phe Gly Trp Thr His Thr Ser Met Lys Lys Asp Asn Arg Ile Tyr Pro
                485                 490                 495
Asp Lys Ile Thr Gln Ile Pro Ala Val Lys Ala Phe Ala Leu Pro Ala
            500                 505                 510
Gly Thr Gly Tyr Ala Gly Gly Tyr Val Thr Ala Gly Pro Gly Tyr Thr
        515                 520                 525
Gly Gly Asp Val Val Thr Leu Pro Tyr Gln Ala Ser Leu Lys Ile Arg
    530                 535                 540
Leu Thr Ser Ala Pro Thr Asn Lys Asn Tyr Arg Val Arg Leu Arg Tyr
545                 550                 555                 560
Ala Ser Gly Gly Pro Gly Pro Phe Arg Val Glu Arg Trp Ser Pro Ser
                565                 570                 575
Ser Val Ser Asn Ala Asn Phe Ser Arg Pro Ala Thr Gly Gly Tyr Ser
            580                 585                 590
Ser Phe Asp Tyr Val Asp Thr Leu Val Thr Thr Phe Asn Gln Ser Gly
        595                 600                 605
Val Glu Ile Ile Ile Gln Asn Leu Ser Gly Tyr His Leu Ile Val Asp
    610                 615                 620
Lys Val Glu Phe Ile Pro Ile Asp Ile Gln Ile Glu Lys Cys Thr Lys
625                 630                 635                 640
Cys Gln Phe Glu Gly Asp Ile Cys Arg Cys Glu Gly Val Gln Ser Leu
                645                 650                 655
Glu Thr Lys Lys Glu Ile Val Asn Ser Leu Phe Ile Asn
            660                 665
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<210> 30
<211> 1176
<212> PRT
<213> Bacillus thuringiensi

<400> 30

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Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
 1               5                  10                  15
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
            20                  25                  30
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
        35                  40                  45
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
    50                  55                  60
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Pro Val Gln Ile
65                  70                  75                  80
Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
                85                  90                  95
Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
            100                 105                 110
Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
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        115                 120                 125
Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
    130                 135                 140
Ile Pro Leu Leu Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
145                 150                 155                 160
Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
                165                 170                 175
Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
            180                 185                 190
Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
        195                 200                 205
Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
    210                 215                 220
Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
225                 230                 235                 240
Leu Asp Ile Val Ala Leu Phe Ser Asn Tyr Asp Ser Arg Arg Tyr Pro
                245                 250                 255
Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
            260                 265                 270
Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Met Ala Gln Arg Ile Glu
        275                 280                 285
Gln Asn Ile Arg Gln Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
    290                 295                 300
Ile Tyr Thr Asp Val His Arg Gly Phe Asn Tyr Trp Ser Gly His Gln
305                 310                 315                 320
Ile Thr Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Ala Phe Pro
                325                 330                 335
Leu Phe Gly Asn Ala Gly Asn Ala Ala Pro Pro Val Leu Val Ser Leu
            340                 345                 350
Thr Gly Leu Gly Ile Phe Arg Thr Leu Ser Ser Pro Leu Tyr Arg Arg
        355                 360                 365
Ile Ile Leu Gly Ser Gly Pro Asn Asn Gln Glu Leu Phe Val Leu Asp
    370                 375                 380
Gly Thr Glu Phe Ser Phe Ala Ser Leu Thr Thr Asn Leu Pro Ser Thr
385                 390                 395                 400
Ile Tyr Arg Gln Arg Gly Thr Val Asp Ser Leu Asp Val Ile Pro Pro
                405                 410                 415
Gln Asp Asn Ser Val Pro Pro Arg Ala Gly Phe Ser His Arg Leu Ser
            420                 425                 430
His Val Thr Met Leu Ser Gln Ala Ala Gly Ala Val Tyr Thr Leu Arg
        435                 440                 445
Ala Pro Thr Phe Ser Trp Gln His Arg Ser Ala Glu Phe Asn Asn Ile
    450                 455                 460
Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr Asn
465                 470                 475                 480
Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly Gly
                485                 490                 495
Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg Val
            500                 505                 510
Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg Tyr
        515                 520                 525
Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg Pro
    530                 535                 540
Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn Leu
545                 550                 555                 560
Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn Phe
                565                 570                 575
Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn Ser
            580                 585                 590
Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu Val
        595                 600                 605
Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val Asn
    610                 615                 620
Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val Thr
625                 630                 635                 640
Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser Asp
                645                 650                 655
Glu Phe Cys Leu Asp Glu Lys Gln Glu Leu Ser Glu Lys Val Lys His
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660 665 670
Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn Phe
675 680 685
Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr Asp
690 695 700
Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val Thr
705 710 715 720
Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys
725 730 735
Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg Gly
740 745 750
Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn
755 760 765
Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp Pro
770 775 780
Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg Cys
785 790 795 800
Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg Asp
805 810 815
Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile Asp
820 825 830
Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile Phe
835 840 845
Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu Phe
850 855 860
Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys Arg
865 870 875 880
Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu Thr
885 890 895
Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe Val
900 905 910
Asn Ser Gln Tyr Asp Gln Leu Gln Ala Asp Thr Asn Ile Ala Met Ile
915 920 925
His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu Pro
930 935 940
Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu Leu
945 950 955 960
Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn Val
965 970 975
Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val Lys
980 985 990
Gly His Val Asp Val Glu Glu Gln Asn Asn Gln Arg Ser Val Leu Val
995 1000 1005
Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys Pro
1010 1015 1020
Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly
1025 1030 1035 1040
Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu Leu
1045 1050 1055
Lys Phe Ser Asn Cys Val Glu Glu Glu Ile Tyr Pro Asn Asn Thr Val
1060 1065 1070
Thr Cys Asn Asp Tyr Thr Val Asn Gln Glu Glu Tyr Gly Gly Ala Tyr
1075 1080 1085
Thr Ser Arg Asn Arg Gly Tyr Asn Glu Ala Pro Ser Val Pro Ala Asp
1090 1095 1100
Tyr Ala Ser Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu
1105 1110 1115 1120
Asn Pro Cys Glu Phe Asn Arg Gly Tyr Arg Asp Tyr Thr Pro Leu Pro
1125 1130 1135
Val Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Lys
1140 1145 1150
Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser
1155 1160 1165
Val Glu Leu Leu Leu Met Glu Glu
1170 1175

<210> 31

<211> 1178
<212> PRT
<213> Bacillus thuringiensi

<400> 31
Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
1 5 10 15
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
20 25 30
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
35 40 45
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
50 55 60
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
65 70 75 80
Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
85 90 95
Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
100 105 110
Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
115 120 125
Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
130 135 140
Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
145 150 155 160
Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
165 170 175
Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
180 185 190
Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
195 200 205
Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
210 215 220
Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
225 230 235 240
Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
245 250 255
Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
260 265 270
Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
275 280 285
Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
290 295 300
Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Tyr Trp Ser Gly His Gln
305 310 315 320
Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
325 330 335
Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
340 345 350
Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
355 360 365
Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
370 375 380
Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
385 390 395 400
Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
405 410 415
Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
420 425 430
Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
435 440 445
Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
450 455 460
Ile Ile Ala Ser Asp Ser Ile Thr Gln Ile Pro Ala Val Lys Gly Asn
465 470 475 480
Phe Leu Phe Asn Gly Ser Val Ile Ser Gly Pro Gly Phe Thr Gly Gly
485 490 495
Asp Leu Val Arg Leu Asn Ser Ser Gly Asn Asn Ile Gln Asn Arg Gly

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                500                 505                 510
Tyr Ile Glu Val Pro Ile His Phe Pro Ser Thr Ser Thr Arg Tyr Arg
        515                 520                 525
Val Arg Val Arg Tyr Ala Ser Val Thr Pro Ile His Leu Asn Val Asn
    530                 535                 540
Trp Gly Asn Ser Ser Ile Phe Ser Asn Thr Val Pro Ala Thr Ala Thr
545                 550                 555                 560
Ser Leu Asp Asn Leu Gln Ser Ser Asp Phe Gly Tyr Phe Glu Ser Ala
                565                 570                 575
Asn Ala Phe Thr Ser Ser Leu Gly Asn Ile Val Gly Val Arg Asn Phe
            580                 585                 590
Ser Gly Thr Ala Gly Val Ile Ile Asp Arg Phe Glu Phe Ile Pro Val
        595                 600                 605
Thr Ala Thr Leu Glu Ala Glu Tyr Asn Leu Glu Arg Ala Gln Lys Ala
    610                 615                 620
Val Asn Ala Leu Phe Thr Ser Thr Asn Gln Leu Gly Leu Lys Thr Asn
625                 630                 635                 640
Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Thr Tyr Leu
                645                 650                 655
Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu Ser Glu Lys Val
            660                 665                 670
Lys His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Ser
        675                 680                 685
Asn Phe Lys Asp Ile Asn Arg Gln Pro Glu Arg Gly Trp Gly Gly Ser
    690                 695                 700
Thr Gly Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr
705                 710                 715                 720
Val Thr Leu Ser Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr
                725                 730                 735
Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Phe Thr Arg Tyr Gln Leu
            740                 745                 750
Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg
        755                 760                 765
Tyr Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu
    770                 775                 780
Trp Pro Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn
785                 790                 795                 800
Arg Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys
                805                 810                 815
Arg Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp
            820                 825                 830
Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val
        835                 840                 845
Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu
    850                 855                 860
Glu Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val
865                 870                 875                 880
Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp
                885                 890                 895
Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu
            900                 905                 910
Phe Val Asn Ser Gln Tyr Asp Gln Leu Gln Ala Asp Thr Asn Ile Ala
        915                 920                 925
Met Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr
    930                 935                 940
Leu Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu
945                 950                 955                 960
Glu Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg
                965                 970                 975
Asn Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn
            980                 985                 990
Val Lys Gly His Val Asp Val Glu Glu Gln Asn Asn Gln Arg Ser Val
        995                 1000                1005
Leu Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val
    1010                1015                1020
Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly
1025                1030                1035                1040
Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp
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                1045                1050                1055
Glu Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Ile Tyr Pro Asn Asn
            1060                1065                1070
Thr Val Thr Cys Asn Asp Tyr Thr Val Asn Gln Glu Glu Tyr Gly Gly
        1075                1080                1085
Ala Tyr Thr Ser Arg Asn Arg Gly Tyr Asn Glu Ala Pro Ser Val Pro
    1090                1095                1100
Ala Asp Tyr Ala Ser Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg
1105                1110                1115                1120
Arg Glu Asn Pro Cys Glu Phe Asn Arg Gly Tyr Arg Asp Tyr Thr Pro
                1125                1130                1135
Leu Pro Val Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr
            1140                1145                1150
Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val
        1155                1160                1165
Asp Ser Val Glu Leu Leu Leu Met Glu Glu
    1170                1175


<210> 32
<211> 1189
<212> PRT
<213> Bacillus thuringiensi

<400> 32
Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser
 1                5                  10                  15
Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn
            20                  25                  30
Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn
        35                  40                  45
Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp
    50                  55                  60
Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu
65                  70                  75                  80
Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile
                85                  90                  95
Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala
            100                 105                 110
Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg
        115                 120                 125
Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile
    130                 135                 140
Pro Ser Phe Arg Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr
145                 150                 155                 160
Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile
                165                 170                 175
Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr
            180                 185                 190
Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn
        195                 200                 205
Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp
    210                 215                 220
Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu
225                 230                 235                 240
Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile
                245                 250                 255
Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile
            260                 265                 270
Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn
        275                 280                 285
Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu
    290                 295                 300
Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe
305                 310                 315                 320
Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Gly Asn
                325                 330                 335
Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg
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            340                 345                 350
Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr
        355                 360                 365
Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg
    370                 375                 380
Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr
385                 390                 395                 400
Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp
                405                 410                 415
Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala
            420                 425                 430
Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val
        435                 440                 445
Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro
    450                 455                 460
Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly
465                 470                 475                 480
Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu
                485                 490                 495
Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn
            500                 505                 510
Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser
        515                 520                 525
Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val
    530                 535                 540
Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile
545                 550                 555                 560
Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn
                565                 570                 575
Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln
            580                 585                 590
Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp
        595                 600                 605
Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp
    610                 615                 620
Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn
625                 630                 635                 640
Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val
                645                 650                 655
Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys
            660                 665                 670
Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu
        675                 680                 685
Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro
    690                 695                 700
Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp
705                 710                 715                 720
Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu
                725                 730                 735
Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys
            740                 745                 750
Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp
        755                 760                 765
Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn
    770                 775                 780
Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile
785                 790                 795                 800
Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn
                805                 810                 815
Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His
            820                 825                 830
Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn
        835                 840                 845
Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly
    850                 855                 860
His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu
865                 870                 875                 880
Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp
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                885                 890                 895
Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala
            900                 905                 910
Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu
        915                 920                 925
Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val
    930                 935                 940
His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly
945                 950                 955                 960
Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala
                965                 970                 975
Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn
            980                 985                 990
Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu
        995                 1000                1005
Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu
    1010                1015                1020
Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg
1025                1030                1035                1040
Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His
                1045                1050                1055
Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu
            1060                1065                1070
Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly
        1075                1080                1085
Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr
    1090                1095                1100
Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser
1105                1110                1115                1120
Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys
                1125                1130                1135
Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
            1140                1145                1150
Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile
        1155                1160                1165
Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
    1170                1175                1180
Leu Leu Met Glu Glu
1185
```

<210> 33
<211> 719
<212> PRT
<213> Bacillus thuringiensi

<400> 33

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Met Lys Leu Lys Asn Gln Asp Lys His Gln Ser Phe Ser Ser Asn Ala
 1                5                  10                  15
Lys Val Asp Lys Ile Ser Thr Asp Ser Leu Lys Asn Glu Thr Asp Ile
            20                  25                  30
Glu Leu Gln Asn Ile Asn His Glu Asp Cys Leu Lys Met Ser Glu Tyr
        35                  40                  45
Glu Asn Val Glu Pro Phe Val Ser Ala Ser Thr Ile Gln Thr Gly Ile
    50                  55                  60
Gly Ile Ala Gly Lys Ile Leu Gly Thr Leu Gly Val Pro Phe Ala Gly
65                  70                  75                  80
Gln Val Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu Trp Pro Lys
                85                  90                  95
Gly Lys Asn Gln Trp Glu Ile Phe Met Glu His Val Glu Glu Ile Ile
            100                 105                 110
Asn Gln Lys Ile Ser Thr Tyr Ala Arg Asn Lys Ala Leu Thr Asp Leu
        115                 120                 125
Lys Gly Leu Gly Asp Ala Leu Ala Val Tyr His Asp Ser Leu Glu Ser
    130                 135                 140
Trp Val Gly Asn Arg Asn Asn Thr Arg Ala Arg Ser Val Val Lys Ser
145                 150                 155                 160
Gln Tyr Ile Ala Leu Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe
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                 165                 170                 175
Ala Val Ser Gly Glu Glu Val Pro Leu Leu Pro Ile Tyr Ala Gln Ala
            180                 185                 190
Ala Asn Leu His Leu Leu Leu Leu Arg Asp Ala Ser Ile Phe Gly Lys
        195                 200                 205
Glu Trp Gly Leu Ser Ser Ser Glu Ile Ser Thr Phe Tyr Asn Arg Gln
    210                 215                 220
Val Glu Arg Ala Gly Asp Tyr Ser Asp His Cys Val Lys Trp Tyr Ser
225                 230                 235                 240
Thr Gly Leu Asn Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Val Arg
                245                 250                 255
Tyr Asn Gln Phe Arg Arg Asp Met Thr Leu Met Val Leu Asp Leu Val
            260                 265                 270
Ala Leu Phe Pro Ser Tyr Asp Thr Gln Met Tyr Pro Ile Lys Thr Thr
        275                 280                 285
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Ala Ile Gly Thr Val His
    290                 295                 300
Pro His Pro Ser Phe Thr Ser Thr Thr Trp Tyr Asn Asn Asn Ala Pro
305                 310                 315                 320
Ser Phe Ser Ala Ile Glu Ala Ala Val Val Arg Asn Pro His Leu Leu
                325                 330                 335
Asp Phe Leu Glu Gln Val Thr Ile Tyr Ser Leu Leu Ser Arg Trp Ser
            340                 345                 350
Asn Thr Gln Tyr Met Asn Met Trp Gly Gly His Lys Leu Glu Phe Arg
        355                 360                 365
Thr Ile Gly Gly Thr Leu Asn Ile Ser Thr Gln Gly Ser Thr Asn Thr
    370                 375                 380
Ser Ile Asn Pro Val Thr Leu Pro Phe Thr Ser Arg Asp Val Tyr Arg
385                 390                 395                 400
Thr Glu Ser Leu Ala Gly Leu Asn Leu Phe Leu Thr Gln Pro Val Asn
                405                 410                 415
Gly Val Pro Arg Val Asp Phe His Trp Lys Phe Val Thr His Pro Ile
            420                 425                 430
Ala Ser Asp Asn Phe Tyr Tyr Pro Gly Tyr Ala Gly Ile Gly Thr Gln
        435                 440                 445
Leu Gln Asp Ser Glu Asn Glu Leu Pro Pro Glu Ala Thr Gly Gln Pro
    450                 455                 460
Asn Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile Ser
465                 470                 475                 480
Ala Ser His Val Lys Ala Leu Val Tyr Ser Trp Thr His Arg Ser Ala
                485                 490                 495
Asp Arg Thr Asn Thr Ile Glu Pro Asn Ser Ile Thr Gln Ile Pro Leu
            500                 505                 510
Val Lys Ala Phe Asn Leu Ser Ser Gly Ala Ala Val Val Arg Gly Pro
        515                 520                 525
Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe
    530                 535                 540
Gly Asp Ile Arg Val Asn Ile Asn Pro Pro Phe Ala Gln Arg Tyr Arg
545                 550                 555                 560
Val Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe His Thr Ser
                565                 570                 575
Ile Asn Gly Lys Ala Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Asn
            580                 585                 590
Arg Gly Glu Asp Leu Asp Tyr Lys Thr Phe Arg Thr Val Gly Phe Thr
        595                 600                 605
Thr Pro Phe Ser Phe Leu Asp Val Gln Ser Thr Phe Thr Ile Gly Ala
    610                 615                 620
Trp Asn Phe Ser Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe
625                 630                 635                 640
Val Pro Val Glu Val Thr Tyr Glu Ala Glu Tyr Asp Phe Glu Lys Ala
                645                 650                 655
Gln Glu Lys Val Thr Ala Leu Phe Thr Ser Thr Asn Pro Arg Gly Leu
            660                 665                 670
Lys Thr Asp Val Lys Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val
        675                 680                 685
Glu Ser Leu Ser Asp Glu Phe Tyr Leu Asp Glu Lys Arg Glu Leu Phe
    690                 695                 700
Glu Ile Val Lys Tyr Ala Lys Gln Leu His Ile Glu Arg Asn Met
```

705 710 715

<210> 34
<211> 633
<212> PRT
<213> Bacillus thuringiensi

<400> 34
Met Asn Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala Tyr
1 5 10 15
Asn Val Val Ala His Asp Pro Phe Ser Phe Glu His Lys Ser Leu Asp
20 25 30
Thr Ile Gln Lys Glu Trp Met Glu Trp Lys Arg Thr Asp His Ser Leu
35 40 45
Tyr Val Ala Pro Val Val Gly Thr Val Ser Ser Phe Leu Leu Lys Lys
50 55 60
Val Gly Ser Leu Ile Gly Lys Arg Ile Leu Ser Glu Leu Trp Gly Ile
65 70 75 80
Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg Glu
85 90 95
Thr Glu Gln Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala Arg
100 105 110
Val Asn Ala Glu Leu Ile Gly Leu Gln Ala Asn Ile Arg Glu Phe Asn
115 120 125
Gln Gln Val Asp Asn Phe Leu Asn Pro Thr Gln Asn Pro Val Pro Leu
130 135 140
Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn Arg
145 150 155 160
Leu Pro Gln Phe Gln Ile Gln Gly Tyr Gln Leu Leu Leu Leu Pro Leu
165 170 175
Phe Ala Gln Ala Ala Asn Met His Leu Ser Phe Ile Arg Asp Val Ile
180 185 190
Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr Tyr
195 200 205
Arg Asp Tyr Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys Ile
210 215 220
Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His Asp
225 230 235 240
Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr Val
245 250 255
Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Met Val Ser Ser Gly
260 265 270
Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser Phe
275 280 285
Thr Ala Gln Asn Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn Ser
290 295 300
Asn Tyr Ile Leu Ser Gly Ile Ser Gly Thr Arg Leu Ser Ile Thr Phe
305 310 315 320
Pro Asn Ile Gly Gly Leu Pro Gly Ser Thr Thr Thr His Ser Leu Asn
325 330 335
Ser Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Leu Ile Gly
340 345 350
Ala Thr Asn Leu Asn His Asn Phe Asn Cys Ser Thr Val Leu Pro Pro
355 360 365
Leu Ser Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Thr Asp Arg
370 375 380
Glu Gly Val Ala Thr Ser Thr Asn Trp Gln Thr Glu Ser Phe Gln Thr
385 390 395 400
Thr Leu Ser Leu Arg Cys Gly Ala Phe Ser Ala Arg Gly Asn Ser Asn
405 410 415
Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu Val
420 425 430
Ile Arg Asn Glu Asp Leu Thr Arg Pro Leu His Tyr Asn Gln Ile Arg
435 440 445
Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr Leu
450 455 460
Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Ala Asn Glu Asn

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465                 470                 475                 480
Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr Ile
                485                 490                 495
Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe Ile
            500                 505                 510
Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln Ser
        515                 520                 525
Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr Asn
    530                 535                 540
Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val Thr
545                 550                 555                 560
Ile Asn Gly Arg Val Tyr Thr Val Ser Asn Val Asn Thr Thr Thr Asn
                565                 570                 575
Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn Ile
            580                 585                 590
Gly Asn Ile Val Ala Ser Asp Asn Thr Asn Val Thr Leu Asp Ile Asn
        595                 600                 605
Val Thr Leu Asn Ser Gly Thr Pro Phe Asp Leu Met Asn Ile Met Phe
    610                 615                 620
Val Pro Thr Asn Leu Pro Pro Leu Tyr
625                 630


<210> 35
<211> 652
<212> PRT
<213> Bacillus thuringiensi

<400> 35
Met Ile Arg Lys Gly Gly Arg Lys Met Asn Pro Asn Asn Arg Ser Glu
 1                5                  10                  15
His Asp Thr Ile Lys Thr Thr Glu Asn Asn Glu Val Pro Thr Asn His
            20                  25                  30
Val Gln Tyr Pro Leu Ala Glu Thr Pro Asn Pro Thr Leu Glu Asp Leu
        35                  40                  45
Asn Tyr Lys Glu Phe Leu Arg Met Thr Ala Asp Asn Asn Thr Glu Ala
    50                  55                  60
Leu Asp Ser Ser Thr Thr Lys Asp Val Ile Gln Lys Gly Ile Ser Val
65                  70                  75                  80
Val Gly Asp Leu Leu Gly Val Val Gly Phe Pro Phe Gly Gly Ala Leu
                85                  90                  95
Val Ser Phe Tyr Thr Asn Phe Leu Asn Thr Ile Trp Pro Ser Glu Asp
            100                 105                 110
Pro Trp Lys Ala Phe Met Glu Gln Val Glu Ala Leu Met Asp Gln Lys
        115                 120                 125
Ile Ala Asp Tyr Ala Lys Asn Lys Ala Leu Ala Glu Leu Gln Gly Leu
    130                 135                 140
Gln Asn Asn Val Glu Asp Tyr Val Ser Ala Leu Ser Ser Trp Gln Lys
145                 150                 155                 160
Asn Pro Val Ser Ser Arg Asn Pro His Ser Gln Gly Arg Ile Arg Glu
                165                 170                 175
Leu Phe Ser Gln Ala Glu Ser His Phe Arg Asn Ser Met Pro Ser Phe
            180                 185                 190
Ala Ile Ser Gly Tyr Glu Val Leu Phe Leu Thr Thr Tyr Ala Gln Ala
        195                 200                 205
Ala Asn Thr His Leu Phe Leu Leu Lys Asp Ala Gln Ile Tyr Gly Glu
    210                 215                 220
Glu Trp Gly Tyr Glu Lys Glu Asp Ile Ala Glu Phe Tyr Lys Arg Gln
225                 230                 235                 240
Leu Lys Leu Thr Gln Glu Tyr Thr Asp His Cys Val Lys Trp Tyr Asn
                245                 250                 255
Val Gly Leu Asp Lys Leu Arg Gly Ser Ser Tyr Glu Ser Trp Val Asn
            260                 265                 270
Phe Asn Arg Tyr Arg Arg Glu Met Thr Leu Thr Val Leu Asp Leu Ile
        275                 280                 285
Ala Leu Phe Pro Leu Tyr Asp Val Arg Leu Tyr Pro Lys Glu Val Lys
    290                 295                 300
Thr Glu Leu Thr Arg Asp Val Leu Thr Asp Pro Ile Val Gly Val Asn
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305 310 315 320
Asn Leu Arg Gly Tyr Gly Thr Thr Phe Ser Asn Ile Glu Asn Tyr Ile
325 330 335
Arg Lys Pro His Leu Phe Asp Tyr Leu His Arg Ile Gln Phe His Thr
340 345 350
Arg Phe Gln Pro Gly Tyr Tyr Gly Asn Asp Ser Phe Asn Tyr Trp Ser
355 360 365
Gly Asn Tyr Val Ser Thr Arg Pro Ser Ile Gly Ser Asn Asp Ile Ile
370 375 380
Thr Ser Pro Phe Tyr Gly Asn Lys Ser Ser Glu Pro Val Gln Asn Leu
385 390 395 400
Glu Phe Asn Gly Glu Lys Val Tyr Arg Ala Val Ala Asn Thr Asn Leu
405 410 415
Ala Val Trp Pro Ser Ala Val Tyr Ser Gly Val Thr Lys Val Glu Phe
420 425 430
Ser Gln Tyr Asn Asp Gln Thr Asp Glu Ala Ser Thr Gln Thr Tyr Asp
435 440 445
Ser Lys Arg Asn Val Gly Ala Val Ser Trp Asp Ser Ile Asp Gln Leu
450 455 460
Pro Pro Glu Thr Thr Asp Glu Pro Leu Glu Lys Gly Tyr Ser His Gln
465 470 475 480
Leu Asn Tyr Val Met Cys Phe Leu Met Gln Gly Ser Arg Gly Thr Ile
485 490 495
Pro Val Leu Thr Trp Thr His Lys Ser Val Asp Phe Phe Asn Met Ile
500 505 510
Asp Ser Lys Lys Ile Thr Gln Leu Pro Leu Val Lys Ala Tyr Lys Leu
515 520 525
Gln Ser Gly Ala Ser Val Val Ala Gly Pro Arg Phe Thr Gly Gly Asp
530 535 540
Ile Ile Gln Cys Thr Glu Asn Gly Ser Ala Ala Thr Ile Tyr Val Thr
545 550 555 560
Pro Asp Val Ser Tyr Ser Gln Lys Tyr Arg Ala Arg Ile His Tyr Ala
565 570 575
Ser Thr Ser Gln Ile Thr Phe Thr Leu Ser Leu Asp Gly Ala Pro Phe
580 585 590
Asn Gln Tyr Tyr Phe Asp Lys Thr Ile Asn Lys Gly Asp Thr Leu Thr
595 600 605
Tyr Asn Ser Phe Asn Leu Ala Ser Phe Ser Thr Pro Phe Glu Leu Ser
610 615 620
Gly Asn Asn Leu Gln Ile Gly Val Thr Gly Leu Ser Ala Gly Asp Lys
625 630 635 640
Val Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Asn
645 650

<210> 36
<211> 659
<212> PRT
<213> Bacillus thuringiensi

<400> 36
Met Ile Arg Met Gly Gly Arg Lys Met Asn Pro Asn Asn Arg Ser Glu
1 5 10 15
Tyr Asp Thr Ile Lys Val Thr Pro Asn Ser Glu Leu Pro Thr Asn His
20 25 30
Asn Gln Tyr Pro Leu Ala Asp Asn Pro Asn Ser Thr Leu Glu Glu Leu
35 40 45
Asn Tyr Lys Glu Phe Leu Arg Met Thr Ala Asp Asn Ser Thr Glu Val
50 55 60
Leu Asp Ser Ser Thr Val Lys Asp Ala Val Gly Thr Gly Ile Ser Val
65 70 75 80
Val Gly Gln Ile Leu Gly Val Val Gly Val Pro Phe Ala Gly Ala Leu
85 90 95
Thr Ser Phe Tyr Gln Ser Phe Leu Asn Ala Ile Trp Pro Ser Asp Ala
100 105 110
Asp Pro Trp Lys Ala Phe Met Ala Gln Val Glu Val Leu Ile Asp Lys
115 120 125
Lys Ile Glu Glu Tyr Ala Lys Ser Lys Ala Leu Ala Glu Leu Gln Gly

```
    130                 135                 140
Leu Gln Asn Asn Phe Glu Asp Tyr Val Asn Ala Leu Asp Ser Trp Lys
145                 150                 155                 160
Lys Ala Pro Val Asn Leu Arg Ser Arg Arg Ser Gln Asp Arg Ile Arg
                165                 170                 175
Glu Leu Phe Ser Gln Ala Glu Ser His Phe Arg Asn Ser Met Pro Ser
            180                 185                 190
Phe Ala Val Ser Lys Phe Glu Val Leu Phe Leu Pro Thr Tyr Ala Gln
        195                 200                 205
Ala Ala Asn Thr His Leu Leu Leu Leu Lys Asp Ala Gln Val Phe Gly
    210                 215                 220
Glu Glu Trp Gly Tyr Ser Ser Glu Asp Ile Ala Glu Phe Tyr Gln Arg
225                 230                 235                 240
Gln Leu Lys Leu Thr Gln Gln Tyr Thr Asp His Cys Val Asn Trp Tyr
                245                 250                 255
Asn Val Gly Leu Asn Ser Leu Arg Gly Ser Thr Tyr Asp Ala Trp Val
            260                 265                 270
Lys Phe Asn Arg Phe Arg Arg Glu Met Thr Leu Thr Val Leu Asp Leu
        275                 280                 285
Ile Val Leu Phe Pro Phe Tyr Asp Val Arg Leu Tyr Ser Lys Gly Val
    290                 295                 300
Lys Thr Glu Leu Thr Arg Asp Ile Phe Thr Asp Pro Ile Phe Thr Leu
305                 310                 315                 320
Asn Ala Leu Gln Glu Tyr Gly Pro Thr Phe Ser Ser Ile Glu Asn Ser
                325                 330                 335
Ile Arg Lys Pro His Leu Phe Asp Tyr Leu Arg Gly Ile Glu Phe His
            340                 345                 350
Thr Arg Leu Arg Pro Gly Tyr Ser Gly Lys Asp Ser Phe Asn Tyr Trp
        355                 360                 365
Ser Gly Asn Tyr Val Glu Thr Arg Pro Ser Ile Gly Ser Asn Asp Thr
    370                 375                 380
Ile Thr Ser Pro Phe Tyr Gly Asp Lys Ser Ile Glu Pro Ile Gln Lys
385                 390                 395                 400
Leu Ser Phe Asp Gly Gln Lys Val Tyr Arg Thr Ile Ala Asn Thr Asp
                405                 410                 415
Ile Ala Ala Phe Pro Asp Gly Lys Ile Tyr Phe Gly Val Thr Lys Val
            420                 425                 430
Asp Phe Ser Gln Tyr Asp Asp Gln Lys Asn Glu Thr Ser Thr Gln Thr
        435                 440                 445
Tyr Asp Ser Lys Arg Tyr Asn Gly Tyr Leu Gly Ala Gln Asp Ser Ile
    450                 455                 460
Asp Gln Leu Pro Pro Glu Thr Thr Asp Glu Pro Leu Glu Lys Ala Tyr
465                 470                 475                 480
Ser His Gln Leu Asn Tyr Ala Glu Cys Phe Leu Met Gln Asp Arg Arg
                485                 490                 495
Gly Thr Ile Pro Phe Phe Thr Trp Thr His Arg Ser Val Asp Phe Phe
            500                 505                 510
Asn Thr Ile Asp Ala Glu Lys Ile Thr Gln Leu Pro Val Val Lys Ala
        515                 520                 525
Tyr Ala Leu Ser Ser Gly Ala Ser Ile Ile Glu Gly Pro Gly Phe Thr
    530                 535                 540
Gly Gly Asn Leu Leu Phe Leu Lys Glu Ser Ser Asn Ser Ile Ala Lys
545                 550                 555                 560
Phe Lys Val Thr Leu Asn Ser Ala Ala Leu Leu Gln Arg Tyr Arg Val
                565                 570                 575
Arg Ile Arg Tyr Ala Ser Thr Thr Asn Leu Arg Leu Phe Val Gln Asn
            580                 585                 590
Ser Asn Asn Asp Phe Leu Val Ile Tyr Ile Asn Lys Thr Met Asn Ile
        595                 600                 605
Asp Gly Asp Leu Thr Tyr Gln Thr Phe Asp Phe Ala Thr Ser Asn Ser
    610                 615                 620
Asn Met Gly Phe Ser Gly Asp Thr Asn Asp Phe Ile Ile Gly Ala Glu
625                 630                 635                 640
Ser Phe Val Ser Asn Glu Lys Ile Tyr Ile Asp Lys Ile Glu Phe Ile
                645                 650                 655
Pro Val Gln
```

<210> 37
<211> 652
<212> PRT
<213> Bacillus thuringiensi

<400> 37
Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
1 5 10 15
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
20 25 30
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
35 40 45
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
50 55 60
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
65 70 75 80
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
85 90 95
Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
100 105 110
Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser
115 120 125
Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr
130 135 140
Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser
145 150 155 160
Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser
165 170 175
His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
180 185 190
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
195 200 205
Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu
210 215 220
Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr
225 230 235 240
Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
245 250 255
Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu
260 265 270
Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp
275 280 285
Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile
290 295 300
Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro
305 310 315 320
Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp
325 330 335
Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe
340 345 350
Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg
355 360 365
Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp
370 375 380
Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val
385 390 395 400
Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
405 410 415
Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
420 425 430
Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
435 440 445
His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr
450 455 460
Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu
465 470 475 480
Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp

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                485                 490                 495
Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
            500                 505                 510
Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser
        515                 520                 525
Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys
    530                 535                 540
Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala
545                 550                 555                 560
Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
                565                 570                 575
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile
            580                 585                 590
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr
        595                 600                 605
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys
    610                 615                 620
Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile
625                 630                 635                 640
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu
                645                 650
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<210> 38
<211> 1180
<212> PRT
<213> Bacillus thuringiensi

<400> 38

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Met Asn Pro Tyr Gln Asn Lys Asn Glu Tyr Glu Thr Leu Asn Ala Ser
 1               5                  10                  15
Gln Lys Lys Leu Asn Ile Ser Asn Asn Tyr Thr Arg Tyr Pro Ile Glu
            20                  25                  30
Asn Ser Pro Lys Gln Leu Leu Gln Ser Thr Asn Tyr Lys Asp Trp Leu
        35                  40                  45
Asn Met Cys Gln Gln Asn Gln Gln Tyr Gly Gly Asp Phe Glu Thr Phe
    50                  55                  60
Ile Asp Ser Gly Glu Leu Ser Ala Tyr Thr Ile Val Val Gly Thr Val
65                  70                  75                  80
Leu Thr Gly Phe Gly Phe Thr Thr Pro Leu Gly Leu Ala Leu Ile Gly
                85                  90                  95
Phe Gly Thr Leu Ile Pro Val Leu Phe Pro Ala Gln Asp Gln Ser Asn
            100                 105                 110
Thr Trp Ser Asp Phe Ile Thr Gln Thr Lys Asn Ile Ile Lys Lys Glu
        115                 120                 125
Ile Ala Ser Thr Tyr Ile Ser Asn Ala Asn Lys Ile Leu Asn Arg Ser
    130                 135                 140
Phe Asn Val Ile Ser Thr Tyr His Asn His Leu Lys Thr Trp Glu Asn
145                 150                 155                 160
Asn Pro Asn Pro Gln Asn Thr Gln Asp Val Arg Thr Gln Ile Gln Leu
                165                 170                 175
Val His Tyr His Phe Gln Asn Val Ile Pro Glu Leu Val Asn Ser Cys
            180                 185                 190
Pro Pro Asn Pro Ser Asp Cys Asp Tyr Tyr Asn Ile Leu Val Leu Ser
        195                 200                 205
Ser Tyr Ala Gln Ala Ala Asn Leu His Leu Thr Val Leu Asn Gln Ala
    210                 215                 220
Val Lys Phe Glu Ala Tyr Leu Lys Asn Asn Arg Gln Phe Asp Tyr Leu
225                 230                 235                 240
Glu Pro Leu Pro Thr Ala Ile Asp Tyr Tyr Pro Val Leu Thr Lys Ala
                245                 250                 255
Ile Glu Asp Tyr Thr Asn Tyr Cys Val Thr Thr Tyr Lys Lys Gly Leu
            260                 265                 270
Asn Leu Ile Lys Thr Thr Pro Asp Ser Asn Leu Asp Gly Asn Ile Asn
        275                 280                 285
Trp Asn Thr Tyr Asn Thr Tyr Arg Thr Lys Met Thr Thr Ala Val Leu
    290                 295                 300
Asp Leu Val Ala Leu Phe Pro Asn Tyr Asp Val Gly Lys Tyr Pro Ile
```

305 310 315 320
Gly Val Gln Ser Glu Leu Thr Arg Glu Ile Tyr Gln Val Leu Asn Phe
325 330 335
Glu Glu Ser Pro Tyr Lys Tyr Tyr Asp Phe Gln Tyr Gln Glu Asp Ser
340 345 350
Leu Thr Arg Arg Pro His Leu Phe Thr Trp Leu Asp Ser Leu Asn Phe
355 360 365
Tyr Glu Lys Ala Gln Thr Thr Pro Asn Asn Phe Phe Thr Ser His Tyr
370 375 380
Asn Met Phe His Tyr Thr Leu Asp Asn Ile Ser Gln Lys Ser Ser Val
385 390 395 400
Phe Gly Asn His Asn Val Thr Asp Lys Leu Lys Ser Leu Gly Leu Ala
405 410 415
Thr Asn Ile Tyr Ile Phe Leu Leu Asn Val Ile Ser Leu Asp Asn Lys
420 425 430
Tyr Leu Asn Asp Tyr Asn Asn Ile Ser Lys Met Asp Phe Phe Ile Thr
435 440 445
Asn Gly Thr Arg Leu Leu Glu Lys Glu Leu Thr Ala Gly Ser Gly Gln
450 455 460
Ile Thr Tyr Asp Val Asn Lys Asn Ile Phe Gly Leu Pro Ile Leu Lys
465 470 475 480
Arg Arg Glu Asn Gln Gly Asn Pro Thr Leu Phe Pro Thr Tyr Asp Asn
485 490 495
Tyr Ser His Ile Leu Ser Phe Ile Lys Ser Leu Ser Ile Pro Ala Thr
500 505 510
Tyr Lys Thr Gln Val Tyr Thr Phe Ala Trp Thr His Ser Ser Val Asp
515 520 525
Pro Lys Asn Thr Ile Tyr Thr His Leu Thr Thr Gln Ile Pro Ala Val
530 535 540
Lys Ala Asn Ser Leu Gly Thr Ala Ser Lys Val Val Gln Gly Pro Gly
545 550 555 560
His Thr Gly Gly Asp Leu Ile Asp Phe Lys Asp His Phe Lys Ile Thr
565 570 575
Cys Gln His Ser Asn Phe Gln Gln Ser Tyr Phe Ile Arg Ile Arg Tyr
580 585 590
Ala Ser Asn Gly Ser Ala Asn Thr Arg Ala Val Ile Asn Leu Ser Ile
595 600 605
Pro Gly Val Ala Glu Leu Gly Met Ala Leu Asn Pro Thr Phe Ser Gly
610 615 620
Thr Asp Tyr Thr Asn Leu Lys Tyr Lys Asp Phe Gln Tyr Leu Glu Phe
625 630 635 640
Ser Asn Glu Val Lys Phe Ala Pro Asn Gln Asn Ile Ser Leu Val Phe
645 650 655
Asn Arg Ser Asp Val Tyr Thr Asn Thr Thr Val Leu Ile Asp Lys Ile
660 665 670
Glu Phe Leu Pro Ile Thr Arg Ser Ile Arg Glu Asp Arg Glu Lys Gln
675 680 685
Lys Leu Glu Thr Val Gln Gln Ile Ile Asn Thr Phe Tyr Ala Asn Pro
690 695 700
Ile Lys Asn Thr Leu Gln Ser Glu Leu Thr Asp Tyr Asp Ile Asp Gln
705 710 715 720
Ala Ala Asn Leu Val Glu Cys Ile Ser Glu Glu Leu Tyr Pro Lys Glu
725 730 735
Lys Met Leu Leu Leu Asp Glu Val Lys Asn Ala Lys Gln Leu Ser Gln
740 745 750
Ser Arg Asn Val Leu Gln Asn Gly Asp Phe Glu Ser Ala Thr Leu Gly
755 760 765
Trp Thr Thr Ser Asp Asn Ile Thr Ile Gln Glu Asp Asp Pro Ile Phe
770 775 780
Lys Gly His Tyr Leu His Met Ser Gly Ala Arg Asp Ile Asp Gly Thr
785 790 795 800
Ile Phe Pro Thr Tyr Ile Phe Gln Lys Ile Asp Glu Ser Lys Leu Lys
805 810 815
Pro Tyr Thr Arg Tyr Leu Val Arg Gly Phe Val Gly Ser Ser Lys Asp
820 825 830
Val Glu Leu Val Val Ser Arg Tyr Gly Glu Glu Ile Asp Ala Ile Met
835 840 845
Asn Val Pro Ala Asp Leu Asn Tyr Leu Tyr Pro Ser Thr Phe Asp Cys

```
    850                 855                 860
Glu Gly Ser Asn Arg Cys Glu Thr Ser Ala Val Pro Ala Asn Ile Gly
865                 870                 875                 880
Asn Thr Ser Asp Met Leu Tyr Ser Cys Gln Tyr Asp Thr Gly Lys Lys
                885                 890                 895
His Val Val Cys Gln Asp Ser His Gln Phe Ser Phe Thr Ile Asp Thr
            900                 905                 910
Gly Ala Leu Asp Thr Asn Glu Asn Ile Gly Val Trp Val Met Phe Lys
        915                 920                 925
Ile Ser Ser Pro Asp Gly Tyr Ala Ser Leu Asp Asn Leu Glu Val Ile
    930                 935                 940
Glu Glu Gly Pro Ile Asp Gly Glu Ala Leu Ser Arg Val Lys His Met
945                 950                 955                 960
Glu Lys Lys Trp Asn Asp Gln Met Glu Ala Lys Arg Ser Glu Thr Gln
                965                 970                 975
Gln Ala Tyr Asp Val Ala Lys Gln Ala Ile Asp Ala Leu Phe Thr Asn
            980                 985                 990
Val Gln Asp Glu Ala Leu Gln Phe Asp Thr Thr Leu Ala Gln Ile Gln
        995                 1000                1005
Tyr Ala Glu Tyr Leu Val Gln Ser Ile Pro Tyr Val Tyr Asn Asp Trp
    1010                1015                1020
Leu Ser Asp Val Pro Gly Met Asn Tyr Asp Ile Tyr Val Glu Leu Asp
1025                1030                1035                1040
Ala Arg Val Ala Gln Ala Arg Tyr Leu Tyr Asp Thr Arg Asn Ile Ile
                1045                1050                1055
Lys Asn Gly Asp Phe Thr Gln Gly Val Met Gly Trp His Val Thr Gly
            1060                1065                1070
Asn Ala Asp Val Gln Gln Ile Asp Gly Val Ser Val Leu Val Leu Ser
        1075                1080                1085
Asn Trp Ser Ala Gly Val Ser Gln Asn Val His Leu Gln His Asn His
    1090                1095                1100
Gly Tyr Val Leu Arg Val Ile Ala Lys Lys Glu Gly Pro Gly Asn Gly
1105                1110                1115                1120
Tyr Val Thr Leu Met Asp Cys Glu Glu Asn Gln Glu Lys Leu Thr Phe
                1125                1130                1135
Thr Ser Cys Glu Glu Gly Tyr Ile Thr Lys Thr Val Asp Val Phe Pro
            1140                1145                1150
Asp Thr Asp Arg Val Arg Ile Glu Ile Gly Glu Thr Glu Gly Ser Phe
        1155                1160                1165
Tyr Ile Glu Ser Ile Glu Leu Ile Cys Met Asn Glu
    1170                1175                1180


<210> 39
<211> 1136
<212> PRT
<213> Bacillus thuringiensi

<400> 39
Met Asn Ser Gly Tyr Pro Leu Ala Asn Asp Leu Gln Gly Ser Met Lys
 1               5                  10                  15
Asn Thr Asn Tyr Lys Asp Trp Leu Ala Met Cys Glu Asn Asn Gln Gln
            20                  25                  30
Tyr Gly Val Asn Pro Ala Ala Ile Asn Ser Ser Ser Val Ser Thr Ala
        35                  40                  45
Leu Lys Val Ala Gly Ala Ile Leu Lys Phe Val Asn Pro Pro Ala Gly
    50                  55                  60
Thr Val Leu Thr Val Leu Ser Ala Val Leu Pro Ile Leu Trp Pro Thr
65                  70                  75                  80
Asn Thr Pro Thr Pro Glu Arg Val Trp Asn Asp Phe Met Thr Asn Thr
                85                  90                  95
Gly Asn Leu Ile Asp Gln Thr Val Thr Ala Tyr Val Arg Thr Asp Ala
            100                 105                 110
Asn Ala Lys Met Thr Val Val Lys Asp Tyr Leu Asp Gln Tyr Thr Thr
        115                 120                 125
Lys Phe Asn Thr Trp Lys Arg Glu Pro Asn Asn Gln Ser Tyr Arg Thr
    130                 135                 140
Ala Val Ile Thr Gln Phe Asn Leu Thr Ser Ala Lys Leu Arg Glu Thr
```

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145                 150                 155                 160
Ala Val Tyr Phe Ser Asn Leu Val Gly Tyr Glu Leu Leu Leu Leu Pro
                165                 170                 175
Ile Tyr Ala Gln Val Ala Asn Phe Asn Leu Leu Leu Ile Arg Asp Gly
            180                 185                 190
Leu Ile Asn Ala Gln Glu Trp Ser Leu Ala Arg Ser Ala Gly Asp Gln
        195                 200                 205
Leu Tyr Asn Thr Met Val Gln Tyr Thr Lys Glu Tyr Ile Ala His Ser
    210                 215                 220
Ile Thr Trp Tyr Asn Lys Gly Leu Asp Val Leu Arg Asn Lys Ser Asn
225                 230                 235                 240
Gly Gln Trp Ile Thr Phe Asn Asp Tyr Lys Arg Glu Met Thr Ile Gln
                245                 250                 255
Val Leu Asp Ile Leu Ala Leu Phe Ala Ser Tyr Asp Pro Arg Arg Tyr
            260                 265                 270
Pro Ala Asp Lys Ile Asp Asn Thr Lys Leu Ser Lys Thr Glu Phe Thr
        275                 280                 285
Arg Glu Ile Tyr Thr Ala Leu Val Glu Ser Pro Ser Ser Lys Ser Ile
    290                 295                 300
Ala Ala Leu Glu Ala Ala Leu Thr Arg Asp Val His Leu Phe Thr Trp
305                 310                 315                 320
Leu Lys Arg Val Asp Phe Trp Thr Asn Thr Ile Tyr Gln Asp Leu Arg
                325                 330                 335
Phe Leu Ser Ala Asn Lys Ile Gly Phe Ser Tyr Thr Asn Ser Ser Ala
            340                 345                 350
Met Gln Glu Ser Gly Ile Tyr Gly Ser Ser Gly Phe Gly Ser Asn Leu
        355                 360                 365
Thr His Gln Ile Gln Leu Asn Ser Asn Val Tyr Lys Thr Ser Ile Thr
    370                 375                 380
Asp Thr Ser Ser Pro Ser Asn Arg Val Thr Lys Met Asp Phe Tyr Lys
385                 390                 395                 400
Ile Asp Gly Thr Leu Ala Ser Tyr Asn Ser Asn Ile Thr Pro Thr Pro
                405                 410                 415
Glu Gly Leu Arg Thr Thr Phe Phe Gly Phe Ser Thr Asn Glu Asn Thr
            420                 425                 430
Pro Asn Gln Pro Thr Val Asn Asp Tyr Thr His Ile Leu Ser Tyr Ile
        435                 440                 445
Lys Thr Asp Val Ile Asp Tyr Asn Ser Asn Arg Val Ser Phe Ala Trp
    450                 455                 460
Thr His Lys Ile Val Asp Pro Asn Asn Gln Ile Tyr Thr Asp Ala Ile
465                 470                 475                 480
Thr Gln Val Pro Ala Val Lys Ser Asn Phe Leu Asn Ala Thr Ala Lys
                485                 490                 495
Val Ile Lys Gly Pro Gly His Thr Gly Gly Asp Leu Val Ala Leu Thr
            500                 505                 510
Ser Asn Gly Thr Leu Ser Gly Arg Met Glu Ile Gln Cys Lys Thr Ser
        515                 520                 525
Ile Phe Asn Asp Pro Thr Arg Ser Tyr Gly Leu Arg Ile Arg Tyr Ala
    530                 535                 540
Ala Asn Ser Pro Ile Val Leu Asn Val Ser Tyr Val Leu Gln Gly Val
545                 550                 555                 560
Ser Arg Gly Thr Thr Ile Ser Thr Glu Ser Thr Phe Ser Arg Pro Asn
                565                 570                 575
Asn Ile Ile Pro Thr Asp Leu Lys Tyr Glu Glu Phe Arg Tyr Lys Asp
            580                 585                 590
Pro Phe Asp Ala Ile Val Pro Met Arg Leu Ser Ser Asn Gln Leu Ile
        595                 600                 605
Thr Ile Ala Ile Gln Pro Leu Asn Met Thr Ser Asn Asn Gln Val Ile
    610                 615                 620
Ile Asp Arg Ile Glu Ile Ile Pro Ile Thr Gln Ser Val Leu Asp Glu
625                 630                 635                 640
Thr Glu Asn Gln Asn Leu Glu Ser Glu Arg Glu Val Val Asn Ala Leu
                645                 650                 655
Phe Thr Asn Asp Ala Lys Asp Ala Leu Asn Ile Gly Thr Thr Asp Tyr
            660                 665                 670
Asp Ile Asp Gln Ala Ala Asn Leu Val Glu Cys Ile Ser Glu Glu Leu
        675                 680                 685
Tyr Pro Lys Glu Lys Met Leu Leu Leu Asp Glu Val Lys Asn Ala Lys
```

```
    690                 695                 700
Gln Leu Ser Gln Ser Arg Asn Val Leu Gln Asn Gly Asp Phe Glu Ser
705                 710                 715                 720
Ala Thr Leu Gly Trp Thr Thr Ser Asp Asn Ile Thr Ile Gln Glu Asp
                725                 730                 735
Asp Pro Ile Phe Lys Gly His Tyr Leu His Met Ser Gly Ala Arg Asp
            740                 745                 750
Ile Asp Gly Thr Ile Phe Pro Thr Tyr Ile Phe Gln Lys Ile Asp Glu
        755                 760                 765
Ser Lys Leu Lys Pro Tyr Thr Arg Tyr Leu Val Arg Gly Phe Val Gly
    770                 775                 780
Ser Ser Lys Asp Val Glu Leu Val Val Ser Arg Tyr Gly Glu Glu Ile
785                 790                 795                 800
Asp Ala Ile Met Asn Val Pro Ala Asp Leu Asn Tyr Leu Tyr Pro Ser
                805                 810                 815
Thr Phe Asp Cys Glu Gly Ser Asn Arg Cys Glu Thr Ser Ala Val Pro
            820                 825                 830
Ala Asn Ile Gly Asn Thr Ser Asp Met Leu Tyr Ser Cys Gln Tyr Asp
        835                 840                 845
Thr Gly Lys Lys His Val Val Cys Gln Asp Ser His Gln Phe Ser Phe
    850                 855                 860
Thr Ile Asp Thr Gly Ala Leu Asp Thr Asn Glu Asn Ile Gly Val Trp
865                 870                 875                 880
Val Met Phe Lys Ile Ser Ser Pro Asp Gly Tyr Ala Ser Leu Asp Asn
                885                 890                 895
Leu Glu Val Ile Glu Glu Gly Pro Ile Asp Gly Glu Ala Leu Ser Arg
            900                 905                 910
Val Lys His Met Glu Lys Lys Trp Asn Asp Gln Met Glu Ala Lys Arg
        915                 920                 925
Ser Glu Thr Gln Gln Ala Tyr Asp Val Ala Lys Gln Ala Ile Asp Ala
    930                 935                 940
Leu Phe Thr Asn Val Gln Asp Glu Ala Leu Gln Phe Asp Thr Thr Leu
945                 950                 955                 960
Ala Gln Ile Gln Tyr Ala Glu Tyr Leu Val Gln Ser Ile Pro Tyr Val
                965                 970                 975
Tyr Asn Asp Trp Leu Ser Asp Val Pro Gly Met Asn Tyr Asp Ile Tyr
            980                 985                 990
Val Glu Leu Asp Ala Arg Val Ala Gln Ala Arg Tyr Leu Tyr Asp Thr
        995                 1000                1005
Arg Asn Ile Ile Lys Asn Gly Asp Phe Thr Gln Gly Val Met Gly Trp
    1010                1015                1020
His Val Thr Gly Asn Ala Asp Val Gln Gln Ile Asp Gly Val Ser Val
1025                1030                1035                1040
Leu Val Leu Ser Asn Trp Ser Ala Gly Val Ser Gln Asn Val His Leu
                1045                1050                1055
Gln His Asn His Gly Tyr Val Leu Arg Val Ile Ala Lys Lys Glu Gly
            1060                1065                1070
Pro Gly Asn Gly Tyr Val Thr Leu Met Asp Cys Glu Glu Asn Gln Glu
        1075                1080                1085
Lys Leu Thr Phe Thr Ser Cys Glu Glu Gly Tyr Ile Thr Lys Thr Val
    1090                1095                1100
Asp Val Phe Pro Asp Thr Asp Arg Val Arg Ile Glu Ile Gly Glu Thr
1105                1110                1115                1120
Glu Gly Ser Phe Tyr Ile Glu Ser Ile Glu Leu Ile Cys Met Asn Glu
                1125                1130                1135
```

<210> 40
<211> 475
<212> PRT
<213> Bacillus thuringiensi

<400> 40

```
Met Ile Ile Asp Ser Lys Thr Thr Leu Pro Arg His Ser Leu Ile His
 1               5                  10                  15
Thr Ile Lys Leu Asn Ser Asn Lys Lys Tyr Gly Pro Gly Asp Met Thr
            20                  25                  30
Asn Gly Asn Gln Phe Ile Ile Ser Lys Gln Glu Trp Ala Thr Ile Gly
```

```
        35                  40                  45
Ala Tyr Ile Gln Thr Gly Leu Gly Leu Pro Val Asn Glu Gln Gln Leu
    50                  55                  60
Arg Thr His Val Asn Leu Ser Gln Asp Ile Ser Ile Pro Ser Asp Phe
65                  70                  75                  80
Ser Gln Leu Tyr Asp Val Tyr Cys Ser Asp Lys Thr Ser Ala Glu Trp
                85                  90                  95
Trp Asn Lys Asn Leu Tyr Pro Leu Ile Ile Lys Ser Ala Asn Asp Ile
            100                 105                 110
Ala Ser Tyr Gly Phe Lys Val Ala Gly Asp Pro Ser Ile Lys Lys Asp
        115                 120                 125
Gly Tyr Phe Lys Lys Leu Gln Asp Glu Leu Asp Asn Ile Val Asp Asn
    130                 135                 140
Asn Ser Asp Asp Asp Ala Ile Ala Lys Ala Ile Lys Asp Phe Lys Ala
145                 150                 155                 160
Arg Cys Gly Ile Leu Ile Lys Glu Ala Lys Gln Tyr Glu Glu Ala Ala
                165                 170                 175
Lys Asn Ile Val Thr Ser Leu Asp Gln Phe Leu His Gly Asp Gln Lys
            180                 185                 190
Lys Leu Glu Gly Val Ile Asn Ile Gln Lys Arg Leu Lys Glu Val Gln
        195                 200                 205
Thr Ala Leu Asn Gln Ala His Gly Glu Ser Ser Pro Ala His Lys Glu
    210                 215                 220
Leu Leu Glu Lys Val Lys Asn Leu Lys Thr Thr Leu Glu Arg Thr Ile
225                 230                 235                 240
Lys Ala Glu Gln Asp Leu Glu Lys Lys Val Glu Tyr Ser Phe Leu Leu
                245                 250                 255
Gly Pro Leu Leu Gly Phe Val Val Tyr Glu Ile Leu Glu Asn Thr Ala
            260                 265                 270
Val Gln His Ile Lys Asn Gln Ile Asp Glu Ile Lys Lys Gln Leu Asp
        275                 280                 285
Ser Ala Gln His Asp Leu Asp Arg Asp Val Lys Ile Ile Gly Met Leu
    290                 295                 300
Asn Ser Ile Asn Thr Asp Ile Asp Asn Leu Tyr Ser Gln Gly Gln Glu
305                 310                 315                 320
Ala Ile Lys Val Phe Gln Lys Leu Gln Gly Ile Trp Ala Thr Ile Gly
                325                 330                 335
Ala Gln Ile Glu Asn Leu Arg Thr Thr Ser Leu Gln Glu Val Gln Asp
            340                 345                 350
Ser Asp Asp Ala Asp Glu Ile Gln Ile Glu Leu Glu Asp Ala Ser Asp
        355                 360                 365
Ala Trp Leu Val Val Ala Gln Glu Ala Arg Asp Phe Thr Leu Asn Ala
    370                 375                 380
Tyr Ser Thr Asn Ser Arg Gln Asn Leu Pro Ile Asn Val Ile Ser Asp
385                 390                 395                 400
Ser Cys Asn Cys Ser Thr Thr Asn Met Thr Ser Asn Gln Tyr Ser Asn
                405                 410                 415
Pro Thr Thr Asn Met Thr Ser Asn Gln Tyr Met Ile Ser His Glu Tyr
            420                 425                 430
Thr Ser Leu Pro Asn Asn Phe Met Leu Ser Arg Asn Ser Asn Leu Glu
        435                 440                 445
Tyr Lys Cys Pro Glu Asn Asn Phe Met Ile Tyr Trp Tyr Asn Asn Ser
    450                 455                 460
Asp Trp Tyr Asn Asn Ser Asp Trp Tyr Asn Asn
465                 470                 475
```

<210> 41
<211> 1138
<212> PRT
<213> Bacillus thuringiensi

<400> 41

```
Met Asn Leu Asn Asn Leu Asp Gly Tyr Glu Asp Ser Asn Arg Thr Leu
 1               5                  10                  15
Asn Asn Ser Leu Asn Tyr Pro Thr Gln Lys Ala Leu Ser Pro Ser Leu
            20                  25                  30
Lys Asn Met Asn Tyr Gln Asp Phe Leu Ser Ile Thr Glu Arg Glu Gln
```

```
        35                  40                  45
Pro Glu Ala Leu Ala Ser Gly Asn Thr Ala Ile Asn Thr Val Val Ser
    50                  55                  60
Val Thr Gly Ala Thr Leu Ser Ala Leu Gly Val Pro Gly Ala Ser Phe
65                  70                  75                  80
Ile Thr Asn Phe Tyr Leu Lys Ile Ala Gly Leu Leu Trp Pro Glu Asn
                85                  90                  95
Gly Lys Ile Trp Asp Glu Phe Met Thr Glu Val Glu Ala Leu Ile Asp
            100                 105                 110
Gln Lys Ile Glu Glu Tyr Val Arg Asn Lys Ala Ile Ala Glu Leu Asp
        115                 120                 125
Gly Leu Gly Ser Ala Leu Asp Lys Tyr Gln Lys Ala Leu Ala Asp Trp
    130                 135                 140
Leu Gly Lys Gln Asp Asp Pro Glu Ala Ile Leu Ser Val Ala Thr Glu
145                 150                 155                 160
Phe Arg Ile Ile Asp Ser Leu Phe Glu Phe Ser Met Pro Ser Phe Lys
                165                 170                 175
Val Thr Gly Tyr Glu Ile Pro Leu Leu Thr Val Tyr Ala Gln Ala Ala
            180                 185                 190
Asn Leu His Leu Ala Leu Leu Arg Asp Ser Thr Leu Tyr Gly Asp Lys
        195                 200                 205
Trp Gly Phe Thr Gln Asn Asn Ile Glu Glu Asn Tyr Asn Arg Gln Lys
    210                 215                 220
Lys Arg Ile Ser Glu Tyr Ser Asp His Cys Thr Lys Trp Tyr Asn Ser
225                 230                 235                 240
Gly Leu Ser Arg Leu Asn Gly Ser Thr Tyr Glu Gln Trp Ile Asn Tyr
                245                 250                 255
Asn Arg Phe Arg Arg Glu Met Ile Leu Met Ala Leu Asp Leu Val Ala
            260                 265                 270
Val Phe Pro Phe His Asp Pro Arg Arg Tyr Ser Met Glu Thr Ser Thr
        275                 280                 285
Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Val Ser Leu Ser Ile Ser
    290                 295                 300
Asn Pro Asp Ile Gly Pro Ser Phe Ser Gln Met Glu Asn Thr Ala Ile
305                 310                 315                 320
Arg Thr Pro His Leu Val Asp Tyr Leu Asp Glu Leu Tyr Ile Tyr Thr
                325                 330                 335
Ser Lys Tyr Lys Ala Phe Ser His Glu Ile Gln Pro Asp Leu Phe Tyr
            340                 345                 350
Trp Ser Ala His Lys Val Ser Phe Lys Lys Ser Glu Gln Ser Asn Leu
        355                 360                 365
Tyr Thr Thr Gly Ile Tyr Gly Lys Thr Ser Gly Tyr Ile Ser Ser Gly
    370                 375                 380
Ala Tyr Ser Phe His Gly Asn Asp Ile Tyr Arg Thr Leu Ala Ala Pro
385                 390                 395                 400
Ser Val Val Val Tyr Pro Tyr Thr Gln Asn Tyr Gly Val Glu Gln Val
                405                 410                 415
Glu Phe Tyr Gly Val Lys Gly His Val His Tyr Arg Gly Asp Asn Lys
            420                 425                 430
Tyr Asp Leu Thr Tyr Asp Ser Ile Asp Gln Leu Pro Pro Asp Gly Glu
        435                 440                 445
Pro Ile His Glu Lys Tyr Thr His Arg Leu Cys His Ala Thr Ala Ile
    450                 455                 460
Phe Lys Ser Thr Pro Asp Tyr Asp Asn Ala Thr Ile Pro Ile Phe Ser
465                 470                 475                 480
Trp Thr His Arg Ser Ala Glu Tyr Tyr Asn Arg Ile Tyr Pro Asn Lys
                485                 490                 495
Ile Thr Lys Ile Pro Ala Val Lys Met Tyr Lys Leu Asp Asp Pro Ser
            500                 505                 510
Thr Val Val Lys Gly Pro Gly Phe Thr Gly Gly Asp Leu Val Lys Arg
        515                 520                 525
Gly Ser Thr Gly Tyr Ile Gly Asp Ile Lys Ala Thr Val Asn Ser Pro
    530                 535                 540
Leu Ser Gln Lys Tyr Arg Val Arg Val Arg Tyr Ala Thr Asn Val Ser
545                 550                 555                 560
Gly Gln Phe Asn Val Tyr Ile Asn Asp Lys Ile Thr Leu Gln Thr Lys
                565                 570                 575
Phe Gln Asn Thr Val Glu Thr Ile Gly Glu Gly Lys Asp Leu Thr Tyr
```

```
            580                 585                 590
Gly Ser Phe Gly Tyr Ile Glu Tyr Ser Thr Thr Ile Gln Phe Pro Asp
        595                 600                 605
Glu His Pro Lys Ile Thr Leu His Leu Ser Asp Leu Ser Asn Asn Ser
    610                 615                 620
Ser Phe Tyr Val Asp Ser Ile Glu Phe Ile Pro Val Asp Val Asn Tyr
625                 630                 635                 640
Ala Glu Lys Glu Lys Leu Glu Lys Ala Gln Lys Ala Val Asn Thr Leu
                645                 650                 655
Phe Thr Glu Gly Arg Asn Ala Leu Gln Lys Asp Val Thr Asp Tyr Lys
            660                 665                 670
Val Asp Gln Val Ser Ile Leu Val Asp Cys Ile Ser Gly Asp Leu Tyr
        675                 680                 685
Pro Asn Glu Lys Arg Glu Leu Gln Asn Leu Val Lys Tyr Ala Lys Arg
    690                 695                 700
Leu Ser Tyr Ser Arg Asn Leu Leu Leu Asp Pro Thr Phe Asp Ser Ile
705                 710                 715                 720
Asn Ser Ser Glu Glu Asn Gly Trp Tyr Gly Ser Asn Gly Ile Val Ile
                725                 730                 735
Gly Asn Gly Asp Phe Val Phe Lys Gly Asn Tyr Leu Ile Phe Ser Gly
            740                 745                 750
Thr Asn Asp Thr Gln Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu
        755                 760                 765
Ser Lys Leu Lys Glu Tyr Thr Arg Tyr Lys Leu Lys Gly Phe Ile Glu
    770                 775                 780
Ser Ser Gln Asp Leu Glu Ala Tyr Val Ile Arg Tyr Asp Ala Lys His
785                 790                 795                 800
Arg Thr Leu Asp Val Ser Asp Asn Leu Leu Pro Asp Ile Leu Pro Glu
                805                 810                 815
Asn Thr Cys Gly Glu Pro Asn Arg Cys Ala Ala Gln Gln Tyr Leu Asp
            820                 825                 830
Glu Asn Pro Ser Pro Glu Cys Ser Ser Met Gln Asp Gly Ile Leu Ser
        835                 840                 845
Asp Ser His Ser Phe Ser Leu Asn Ile Asp Thr Gly Ser Ile Asn His
    850                 855                 860
Asn Glu Asn Leu Gly Ile Trp Val Leu Phe Lys Ile Ser Thr Leu Glu
865                 870                 875                 880
Gly Tyr Ala Lys Phe Gly Asn Leu Glu Val Ile Glu Asp Gly Pro Val
                885                 890                 895
Ile Gly Glu Ala Leu Ala Arg Val Lys Arg Gln Glu Thr Lys Trp Arg
            900                 905                 910
Asn Lys Leu Ala Gln Leu Thr Thr Glu Thr Gln Ala Ile Tyr Thr Arg
        915                 920                 925
Ala Lys Gln Ala Leu Asp Asn Leu Phe Ala Asn Ala Gln Asp Ser His
    930                 935                 940
Leu Lys Arg Asp Val Thr Phe Ala Glu Ile Ala Ala Ala Arg Lys Ile
945                 950                 955                 960
Val Gln Ser Ile Arg Glu Ala Tyr Met Ser Trp Leu Ser Val Val Pro
                965                 970                 975
Gly Val Asn His Pro Ile Phe Thr Glu Leu Ser Gly Arg Val Gln Arg
            980                 985                 990
Ala Phe Gln Leu Tyr Asp Val Arg Asn Val Val Arg Asn Gly Arg Phe
        995                 1000                1005
Leu Asn Gly Leu Ser Asp Trp Ile Val Thr Ser Asp Val Lys Val Gln
    1010                1015                1020
Glu Glu Asn Gly Asn Asn Val Leu Val Leu Asn Asn Trp Asp Ala Gln
1025                1030                1035                1040
Val Leu Gln Asn Val Lys Leu Tyr Gln Asp Arg Gly Tyr Ile Leu His
                1045                1050                1055
Val Thr Ala Arg Lys Ile Gly Ile Gly Glu Gly Tyr Ile Thr Ile Thr
            1060                1065                1070
Asp Glu Glu Gly His Thr Asp Gln Leu Arg Phe Thr Ala Cys Glu Glu
        1075                1080                1085
Ile Asp Ala Ser Asn Ala Phe Ile Ser Gly Tyr Ile Thr Lys Glu Leu
    1090                1095                1100
Glu Phe Phe Pro Asp Thr Glu Lys Val His Ile Glu Ile Gly Glu Thr
1105                1110                1115                1120
Glu Gly Ile Phe Leu Val Glu Ser Ile Glu Leu Phe Leu Met Glu Glu
```

1125 1130 1135
Leu Cys

<210> 42
<211> 1157
<212> PRT
<213> Bacillus thuringiensi

<400> 42
Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
1 5 10 15
Ser Thr Ser Val Ser Ser Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
20 25 30
Pro Thr Asp Ala Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu Lys Met
35 40 45
Ser Gly Gly Glu Asn Pro Glu Leu Phe Gly Asn Pro Glu Thr Phe Ile
50 55 60
Ser Ser Ser Thr Ile Gln Thr Gly Ile Gly Ile Val Gly Arg Ile Leu
65 70 75 80
Gly Ala Leu Gly Val Pro Phe Ala Ser Gln Ile Ala Ser Phe Tyr Ser
85 90 95
Phe Ile Val Gly Gln Leu Trp Pro Ser Lys Ser Val Asp Ile Trp Gly
100 105 110
Glu Ile Met Glu Arg Val Glu Glu Leu Val Asp Gln Lys Ile Glu Lys
115 120 125
Tyr Val Lys Asp Lys Ala Leu Ala Glu Leu Lys Gly Leu Gly Asn Ala
130 135 140
Leu Asp Val Tyr Gln Gln Ser Leu Glu Asp Trp Leu Glu Asn Arg Asn
145 150 155 160
Asp Ala Arg Thr Arg Ser Val Val Ser Asn Gln Phe Ile Ala Leu Asp
165 170 175
Leu Asn Phe Val Ser Ser Ile Pro Ser Phe Ala Val Ser Gly His Glu
180 185 190
Val Leu Leu Leu Ala Val Tyr Ala Gln Ala Val Asn Leu His Leu Leu
195 200 205
Leu Leu Arg Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Phe Thr Pro
210 215 220
Gly Glu Ile Ser Arg Phe Tyr Asn Arg Gln Val Gln Leu Thr Ala Glu
225 230 235 240
Tyr Ser Asp Tyr Cys Val Lys Trp Tyr Lys Ile Gly Leu Asp Lys Leu
245 250 255
Lys Gly Thr Thr Ser Lys Ser Trp Leu Asn Tyr His Gln Phe Arg Arg
260 265 270
Glu Met Thr Leu Leu Val Leu Asp Leu Val Ala Leu Phe Pro Asn Tyr
275 280 285
Asp Thr His Met Tyr Pro Ile Glu Thr Thr Ala Gln Leu Thr Arg Asp
290 295 300
Val Tyr Thr Asp Pro Ile Ala Phe Asn Ile Val Thr Ser Thr Gly Phe
305 310 315 320
Cys Asn Pro Trp Ser Thr His Ser Gly Ile Leu Phe Tyr Glu Val Glu
325 330 335
Asn Asn Val Ile Arg Pro Pro His Leu Phe Asp Ile Leu Ser Ser Val
340 345 350
Glu Ile Asn Thr Ser Arg Gly Gly Ile Thr Leu Asn Asn Asp Ala Tyr
355 360 365
Ile Asn Tyr Trp Ser Gly His Thr Leu Lys Tyr Arg Arg Thr Ala Asp
370 375 380
Ser Thr Val Thr Tyr Thr Ala Asn Tyr Gly Arg Ile Thr Ser Glu Lys
385 390 395 400
Asn Ser Phe Ala Leu Glu Asp Arg Asp Ile Phe Glu Ile Asn Ser Thr
405 410 415
Val Ala Asn Leu Ala Asn Tyr Tyr Gln Lys Ala Tyr Gly Val Pro Gly
420 425 430
Ser Trp Phe His Met Val Lys Arg Gly Thr Ser Ser Thr Thr Ala Tyr
435 440 445
Leu Tyr Ser Lys Thr His Thr Ala Leu Gln Gly Cys Thr Gln Val Tyr

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    450                 455                 460
Glu Ser Ser Asp Glu Ile Pro Leu Asp Arg Thr Val Pro Val Ala Glu
465                 470                 475                 480
Ser Tyr Ser His Arg Leu Ser His Ile Thr Ser His Ser Phe Ser Lys
                485                 490                 495
Asn Gly Ser Ala Tyr Tyr Gly Ser Phe Pro Val Phe Val Trp Thr His
            500                 505                 510
Thr Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln
        515                 520                 525
Ile Pro Ala Val Lys Gly Asp Met Leu Tyr Leu Gly Gly Ser Val Val
    530                 535                 540
Gln Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Lys Arg Thr Asn Pro
545                 550                 555                 560
Ser Ile Leu Gly Thr Phe Ala Val Thr Val Asn Gly Ser Leu Ser Gln
                565                 570                 575
Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr Asp Phe Glu Phe
            580                 585                 590
Thr Leu Tyr Leu Gly Asp Thr Ile Glu Lys Asn Arg Phe Asn Lys Thr
        595                 600                 605
Met Asp Asn Gly Ala Ser Leu Thr Tyr Glu Thr Phe Lys Phe Ala Ser
    610                 615                 620
Phe Ile Thr Asp Phe Gln Phe Arg Glu Thr Gln Asp Lys Ile Leu Leu
625                 630                 635                 640
Ser Met Gly Asp Phe Ser Ser Gly Gln Glu Val Tyr Ile Asp Arg Ile
                645                 650                 655
Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala Glu Gln Asp Leu Glu
            660                 665                 670
Ala Ala Lys Lys Ala Val Asn Ala Leu Phe Thr Asn Thr Lys Asp Gly
        675                 680                 685
Leu Arg Pro Gly Val Thr Asp Tyr Glu Val Asn Gln Ala Ala Asn Leu
    690                 695                 700
Val Glu Cys Leu Ser Asp Asp Leu Tyr Pro Asn Glu Lys Arg Leu Leu
705                 710                 715                 720
Phe Asp Ala Val Arg Glu Ala Lys Arg Leu Ser Gly Ala Arg Asn Leu
                725                 730                 735
Leu Gln Asp Pro Asp Phe Gln Glu Ile Asn Gly Glu Asn Gly Trp Ala
            740                 745                 750
Ala Ser Thr Gly Ile Glu Ile Val Glu Gly Asp Ala Val Phe Lys Gly
        755                 760                 765
Arg Tyr Leu Arg Leu Pro Gly Ala Arg Glu Ile Asp Thr Glu Thr Tyr
    770                 775                 780
Pro Thr Tyr Leu Tyr Gln Lys Val Glu Glu Gly Val Leu Lys Pro Tyr
785                 790                 795                 800
Thr Arg Tyr Arg Leu Arg Gly Phe Val Gly Ser Ser Gln Gly Leu Glu
                805                 810                 815
Ile Tyr Thr Ile Arg His Gln Thr Asn Arg Ile Val Lys Asn Val Pro
            820                 825                 830
Asp Asp Leu Leu Pro Asp Val Ser Pro Val Asn Ser Asp Gly Ser Ile
        835                 840                 845
Asn Arg Cys Ser Glu Gln Lys Tyr Val Asn Ser Arg Leu Glu Gly Glu
    850                 855                 860
Asn Arg Ser Gly Asp Ala His Glu Phe Ser Leu Pro Ile Asp Ile Gly
865                 870                 875                 880
Glu Leu Asp Tyr Asn Glu Asn Ala Gly Ile Trp Val Gly Phe Lys Ile
                885                 890                 895
Thr Asp Pro Glu Gly Tyr Ala Thr Leu Gly Asn Leu Glu Leu Val Glu
            900                 905                 910
Glu Gly Pro Leu Ser Gly Asp Ala Leu Glu Arg Leu Gln Arg Glu Glu
        915                 920                 925
Gln Gln Trp Lys Ile Gln Met Thr Arg Arg Arg Glu Glu Thr Asp Arg
    930                 935                 940
Arg Tyr Met Ala Ser Lys Gln Ala Val Asp Arg Leu Tyr Ala Asp Tyr
945                 950                 955                 960
Gln Asp Gln Gln Leu Asn Pro Asp Val Glu Ile Thr Asp Leu Thr Ala
                965                 970                 975
Ala Gln Asp Leu Ile Gln Ser Ile Pro Tyr Val Tyr Asn Glu Met Phe
            980                 985                 990
Pro Glu Ile Pro Gly Met Asn Tyr Thr Lys Phe Thr Glu Leu Thr Asp
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```
        995                 1000                1005
Arg Leu Gln Gln Ala Trp Asn Leu Tyr Asp Gln Arg Asn Ala Ile Pro
    1010                1015                1020
Asn Gly Asp Phe Arg Asn Gly Leu Ser Asn Trp Asn Ala Thr Pro Gly
1025                1030                1035                1040
Val Glu Val Gln Gln Ile Asn His Thr Ser Val Leu Val Ile Pro Asn
                1045                1050                1055
Trp Asp Glu Gln Val Ser Gln Gln Phe Thr Val Gln Pro Asn Gln Arg
            1060                1065                1070
Tyr Val Leu Arg Val Thr Ala Arg Lys Glu Gly Val Gly Asn Gly Tyr
        1075                1080                1085
Val Ser Ile Arg Asp Gly Gly Asn Gln Ser Glu Thr Leu Thr Phe Ser
    1090                1095                1100
Ala Ser Asp Tyr Asp Thr Asn Gly Val Tyr Asn Asp Gln Thr Gly Tyr
1105                1110                1115                1120
Ile Thr Lys Thr Val Thr Phe Ile Pro Tyr Thr Asp Gln Met Trp Ile
                1125                1130                1135
Glu Ile Ser Glu Thr Glu Gly Thr Phe Tyr Ile Glu Ser Val Glu Leu
            1140                1145                1150
Ile Val Asp Val Glu
        1155
```

<210> 43
<211> 675
<212> PRT
<213> Bacillus thuringiensi

<400> 43

```
Met Asn Pro Tyr Gln Asn Lys Asn Glu Tyr Glu Ile Phe Asn Ala Pro
 1               5                  10                  15
Ser Asn Gly Phe Ser Lys Ser Asn Asn Tyr Ser Arg Tyr Pro Leu Ala
            20                  25                  30
Asn Lys Pro Asn Gln Pro Leu Lys Asn Thr Asn Tyr Lys Asp Trp Leu
        35                  40                  45
Asn Val Cys Gln Asp Asn Gln Gln Tyr Gly Asn Asn Ala Gly Asn Phe
    50                  55                  60
Ala Ser Ser Glu Thr Ile Val Gly Val Ser Ala Gly Ile Ile Val Val
65                  70                  75                  80
Gly Thr Met Leu Gly Ala Phe Ala Ala Pro Val Leu Ala Ala Gly Ile
                85                  90                  95
Ile Ser Phe Gly Thr Leu Leu Pro Ile Phe Trp Gln Gly Ser Asp Pro
            100                 105                 110
Ala Asn Val Trp Gln Asp Leu Leu Asn Ile Gly Gly Arg Pro Ile Gln
        115                 120                 125
Glu Ile Asp Lys Asn Ile Ile Asn Val Leu Thr Ser Ile Val Thr Pro
    130                 135                 140
Ile Lys Asn Gln Leu Asp Lys Tyr Gln Glu Phe Phe Asp Lys Trp Glu
145                 150                 155                 160
Pro Ala Arg Thr His Ala Asn Ala Lys Ala Val His Asp Leu Phe Thr
                165                 170                 175
Thr Leu Glu Pro Ile Ile Asp Lys Asp Leu Asp Met Leu Lys Asn Asn
            180                 185                 190
Ala Ser Tyr Arg Ile Pro Thr Leu Pro Ala Tyr Ala Gln Ile Ala Thr
        195                 200                 205
Trp His Leu Asn Leu Leu Lys His Ala Ala Thr Tyr Tyr Asn Ile Trp
    210                 215                 220
Leu Gln Asn Gln Gly Ile Asn Pro Ser Thr Phe Asn Ser Ser Asn Tyr
225                 230                 235                 240
Tyr Gln Gly Tyr Leu Lys Arg Lys Ile Gln Glu Tyr Thr Asp Tyr Cys
                245                 250                 255
Ile Gln Thr Tyr Asn Ala Gly Leu Thr Met Ile Arg Thr Asn Thr Asn
            260                 265                 270
Ala Thr Trp Asn Met Tyr Asn Thr Tyr Arg Leu Glu Met Thr Leu Thr
        275                 280                 285
Val Leu Asp Leu Ile Ala Ile Phe Pro Asn Tyr Asp Pro Glu Lys Tyr
    290                 295                 300
Pro Ile Gly Val Lys Ser Glu Leu Ile Arg Glu Val Tyr Thr Asn Val
```

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305                 310                 315                 320
Asn Ser Asp Thr Phe Arg Thr Ile Thr Glu Leu Glu Asn Gly Leu Thr
                325                 330                 335
Arg Asn Pro Thr Leu Phe Thr Trp Ile Asn Gln Gly Arg Phe Tyr Thr
            340                 345                 350
Arg Asn Ser Arg Asp Ile Leu Asp Pro Tyr Asp Ile Phe Ser Phe Thr
        355                 360                 365
Gly Asn Gln Met Ala Phe Thr His Thr Asn Asp Asp Arg Asn Ile Ile
    370                 375                 380
Trp Gly Ala Val His Gly Asn Ile Ile Ser Gln Asp Thr Ser Lys Val
385                 390                 395                 400
Phe Pro Phe Tyr Arg Asn Lys Pro Ile Asp Lys Val Glu Ile Val Arg
                405                 410                 415
His Arg Glu Tyr Ser Asp Ile Ile Tyr Glu Met Ile Phe Phe Ser Asn
            420                 425                 430
Ser Ser Glu Val Phe Arg Tyr Ser Ser Asn Ser Thr Ile Glu Asn Asn
        435                 440                 445
Tyr Lys Arg Thr Asp Ser Tyr Met Ile Pro Lys Gln Thr Trp Lys Asn
    450                 455                 460
Glu Glu Tyr Gly His Thr Leu Ser Tyr Ile Lys Thr Asp Asn Tyr Ile
465                 470                 475                 480
Phe Ser Val Val Arg Glu Arg Arg Arg Val Ala Phe Ser Trp Thr His
                485                 490                 495
Thr Ser Val Asp Phe Gln Asn Thr Ile Asp Leu Asp Asn Ile Thr Gln
            500                 505                 510
Ile His Ala Leu Lys Ala Leu Lys Val Ser Ser Asp Ser Lys Ile Val
        515                 520                 525
Lys Gly Pro Gly His Thr Gly Gly Asp Leu Val Ile Leu Lys Asp Ser
    530                 535                 540
Met Asp Phe Arg Val Arg Phe Leu Lys Asn Val Ser Arg Gln Tyr Gln
545                 550                 555                 560
Val Arg Ile Arg Tyr Ala Thr Asn Ala Pro Lys Thr Thr Val Phe Leu
                565                 570                 575
Thr Gly Ile Asp Thr Ile Ser Val Glu Leu Pro Ser Thr Thr Ser Arg
            580                 585                 590
Gln Asn Pro Asn Ala Thr Asp Leu Thr Tyr Ala Asp Phe Gly Tyr Val
        595                 600                 605
Thr Phe Pro Arg Thr Val Pro Asn Lys Thr Phe Glu Gly Glu Asp Thr
    610                 615                 620
Leu Leu Met Thr Leu Tyr Gly Thr Pro Asn His Ser Tyr Asn Ile Tyr
625                 630                 635                 640
Ile Asp Lys Ile Glu Phe Ile Pro Ile Thr Gln Ser Val Leu Asp Tyr
                645                 650                 655
Thr Glu Lys Gln Asn Ile Glu Lys Thr Gln Lys Ile Val Asn Asp Leu
            660                 665                 670
Phe Val Asn
        675
```

<210> 44
<211> 648
<212> PRT
<213> Bacillus thuringiensi

<400> 44

```
Met His Tyr Tyr Gly Asn Arg Asn Glu Tyr Asp Ile Leu Asn Ala Ser
 1               5                  10                  15
Ser Asn Asp Ser Asn Met Ser Asn Thr Tyr Pro Arg Tyr Pro Leu Ala
            20                  25                  30
Asn Pro Gln Gln Asp Leu Met Gln Asn Thr Asn Tyr Lys Asp Trp Leu
        35                  40                  45
Asn Val Cys Glu Gly Tyr His Ile Glu Asn Pro Arg Glu Ala Ser Val
    50                  55                  60
Arg Ala Gly Leu Gly Lys Gly Leu Gly Ile Val Ser Thr Ile Val Gly
65                  70                  75                  80
Phe Phe Gly Gly Ser Ile Ile Leu Asp Thr Ile Gly Leu Phe Tyr Gln
                85                  90                  95
Ile Ser Glu Leu Leu Trp Pro Glu Asp Asp Thr Gln Gln Tyr Thr Trp
```

```
                100                 105                 110
Gln Asp Ile Met Asn His Val Glu Asp Leu Ile Asp Lys Arg Ile Thr
            115                 120                 125
Glu Val Ile Arg Gly Asn Ala Ile Arg Thr Leu Ala Asp Leu Gln Gly
    130                 135                 140
Lys Val Asp Asp Tyr Asn Asn Trp Leu Lys Lys Trp Lys Asp Asp Pro
145                 150                 155                 160
Lys Ser Thr Gly Asn Leu Ser Thr Leu Val Thr Lys Phe Thr Ala Leu
                165                 170                 175
Asp Ser Asp Phe Asn Gly Ala Ile Arg Thr Val Asn Asn Gln Gly Ser
            180                 185                 190
Pro Gly Tyr Glu Leu Leu Leu Leu Pro Val Tyr Ala Gln Ile Ala Asn
        195                 200                 205
Leu His Leu Leu Leu Leu Arg Asp Ala Gln Ile Tyr Gly Asp Lys Trp
    210                 215                 220
Trp Ser Ala Arg Ala Asn Ala Arg Asp Asn Tyr Tyr Gln Ile Gln Leu
225                 230                 235                 240
Glu Lys Thr Lys Glu Tyr Thr Glu Tyr Cys Ile Asn Trp Tyr Asn Lys
                245                 250                 255
Gly Leu Asn Asp Phe Arg Thr Ala Gly Gln Trp Val Asn Phe Asn Arg
            260                 265                 270
Tyr Arg Arg Glu Met Thr Leu Thr Val Leu Asp Ile Ile Ser Met Phe
        275                 280                 285
Pro Ile Tyr Asp Ala Arg Leu Tyr Pro Thr Glu Val Lys Thr Glu Leu
    290                 295                 300
Thr Arg Glu Ile Tyr Ser Asp Val Ile Asn Gly Glu Ile Tyr Gly Leu
305                 310                 315                 320
Met Thr Pro Tyr Phe Ser Phe Glu Lys Ala Glu Ser Leu Tyr Thr Arg
                325                 330                 335
Ala Pro His Leu Phe Thr Trp Leu Lys Gly Phe Arg Phe Val Thr Asn
            340                 345                 350
Ser Ile Ser Tyr Trp Thr Phe Leu Ser Gly Gly Gln Asn Lys Tyr Ser
        355                 360                 365
Tyr Thr Asn Asn Ser Ser Ile Asn Glu Gly Ser Phe Arg Gly Gln Asp
    370                 375                 380
Thr Asp Tyr Gly Gly Thr Ser Ser Thr Ile Asn Ile Pro Ser Asn Ser
385                 390                 395                 400
Tyr Val Tyr Asn Leu Trp Thr Glu Asn Tyr Glu Tyr Ile Tyr Pro Trp
                405                 410                 415
Gly Asp Pro Val Asn Ile Thr Lys Met Asn Phe Ser Val Thr Asp Asn
            420                 425                 430
Asn Ser Ser Lys Glu Leu Ile Tyr Gly Ala His Arg Thr Asn Lys Pro
        435                 440                 445
Val Val Arg Thr Asp Phe Asp Phe Leu Thr Asn Lys Glu Gly Thr Glu
    450                 455                 460
Leu Ala Lys Tyr Asn Asp Tyr Asn His Ile Leu Ser Tyr Met Leu Ile
465                 470                 475                 480
Asn Gly Glu Thr Phe Gly Gln Lys Arg His Gly Tyr Ser Phe Ala Phe
                485                 490                 495
Thr His Ser Ser Val Asp Pro Asn Asn Thr Ile Ala Ala Asn Lys Ile
            500                 505                 510
Thr Gln Ile Pro Val Val Lys Ala Ser Ser Ile Asn Gly Ser Ile Ser
        515                 520                 525
Ile Glu Lys Gly Pro Gly Phe Thr Gly Gly Asp Leu Val Lys Met Arg
    530                 535                 540
Ala Asp Ser Gly Leu Thr Met Arg Phe Lys Ala Glu Leu Leu Asp Lys
545                 550                 555                 560
Lys Tyr Arg Val Arg Ile Arg Tyr Lys Cys Asn Tyr Ser Ser Lys Leu
                565                 570                 575
Ile Leu Arg Lys Trp Lys Gly Glu Gly Tyr Ile Gln Gln Gln Ile His
            580                 585                 590
Asn Ile Ser Pro Thr Tyr Gly Ala Phe Ser Tyr Leu Glu Ser Phe Thr
        595                 600                 605
Ile Thr Thr Thr Glu Asn Ile Phe Asp Leu Thr Met Glu Val Thr Tyr
    610                 615                 620
Pro Tyr Gly Arg Gln Phe Val Glu Asp Ile Pro Ser Leu Ile Leu Asp
625                 630                 635                 640
Lys Ile Glu Phe Leu Pro Thr Asn
```

645

<210> 45
<211> 682
<212> PRT
<213> Bacillus thuringiensi

<400> 45
Met Asn Ser Tyr Gln Asn Lys Asn Glu Tyr Glu Ile Leu Asp Ala Lys
1 5 10 15
Arg Asn Thr Cys His Met Ser Asn Cys Tyr Pro Lys Tyr Pro Leu Ala
20 25 30
Asn Asp Pro Gln Met Tyr Leu Arg Asn Thr His Tyr Lys Asp Trp Ile
35 40 45
Asn Met Cys Glu Glu Ala Ser Tyr Ala Ser Ser Gly Pro Ser Gln Leu
50 55 60
Phe Lys Val Gly Gly Ser Ile Val Ala Lys Ile Leu Gly Met Ile Pro
65 70 75 80
Glu Val Gly Pro Leu Leu Ser Trp Met Val Ser Leu Phe Trp Pro Thr
85 90 95
Ile Glu Glu Lys Asn Thr Val Trp Glu Asp Met Ile Lys Tyr Val Ala
100 105 110
Asn Leu Leu Lys Gln Glu Leu Thr Asn Asp Thr Leu Asn Arg Ala Thr
115 120 125
Ser Asn Leu Ser Gly Leu Asn Glu Ser Leu Asn Ile Tyr Asn Arg Ala
130 135 140
Leu Ala Ala Trp Lys Gln Asn Lys Asn Asn Phe Ala Ser Gly Glu Leu
145 150 155 160
Ile Arg Ser Tyr Ile Asn Asp Leu His Ile Leu Phe Thr Arg Asp Ile
165 170 175
Gln Ser Asp Phe Ser Leu Gly Gly Tyr Glu Thr Val Leu Leu Pro Ser
180 185 190
Tyr Ala Ser Ala Ala Asn Leu His Leu Leu Leu Leu Arg Asp Val Ala
195 200 205
Ile Tyr Gly Lys Glu Leu Gly Tyr Pro Ser Thr Asp Val Glu Phe Tyr
210 215 220
Tyr Asn Glu Gln Lys Tyr Tyr Thr Glu Lys Tyr Ser Asn Tyr Cys Val
225 230 235 240
Asn Thr Tyr Lys Ser Gly Leu Glu Ser Lys Lys Gln Ile Gly Trp Ser
245 250 255
Asp Phe Asn Arg Tyr Arg Arg Glu Met Thr Leu Ser Val Leu Asp Ile
260 265 270
Val Ala Leu Phe Pro Leu Tyr Asp Thr Gly Leu Tyr Pro Ser Lys Asp
275 280 285
Gly Lys Ile His Val Lys Ala Glu Leu Thr Arg Glu Ile Tyr Ser Asp
290 295 300
Val Ile Asn Asp His Val Tyr Gly Leu Met Val Pro Tyr Ile Ser Phe
305 310 315 320
Glu His Ala Glu Ser Leu Tyr Thr Arg Arg Pro His Ala Phe Thr Trp
325 330 335
Leu Lys Gly Phe Arg Phe Val Thr Asn Ser Ile Asn Ser Trp Thr Phe
340 345 350
Leu Ser Gly Gly Glu Asn Arg Tyr Phe Leu Thr His Gly Glu Gly Thr
355 360 365
Ile Tyr Asn Gly Pro Phe Leu Gly Gln Asp Thr Glu Tyr Gly Gly Thr
370 375 380
Ser Ser Tyr Ile Asp Ile Ser Asn Asn Ser Ser Ile Tyr Asn Leu Trp
385 390 395 400
Thr Lys Asn Tyr Glu Trp Ile Tyr Pro Trp Thr Asp Pro Val Asn Ile
405 410 415
Thr Lys Ile Asn Phe Ser Ile Thr Asp Asn Ser Asn Ser Ser Glu Ser
420 425 430
Ile Tyr Gly Ala Glu Arg Met Asn Lys Pro Thr Val Arg Thr Asp Phe
435 440 445
Asn Phe Leu Leu Asn Arg Ala Gly Asn Gly Pro Thr Thr Tyr Asn Asp
450 455 460
Tyr Asn His Ile Leu Ser Tyr Met Leu Ile Asn Gly Glu Thr Phe Gly

```
465                 470                 475                 480
Gln Lys Arg His Gly Tyr Ser Phe Ala Phe Thr His Ser Ser Val Asp
                485                 490                 495
Arg Tyr Asn Thr Ile Val Pro Asp Lys Ile Val Gln Ile Pro Ala Val
            500                 505                 510
Lys Thr Asn Leu Val Gly Ala Asn Ile Ile Lys Gly Pro Gly His Thr
        515                 520                 525
Gly Gly Asp Leu Leu Lys Leu Glu Tyr Glu Arg Phe Leu Ser Leu Arg
    530                 535                 540
Ile Lys Leu Ile Ala Ser Met Thr Phe Arg Ile Arg Ile Arg Tyr Ala
545                 550                 555                 560
Ser Asn Ile Ser Gly Gln Met Met Ile Asn Ile Gly Tyr Gln Asn Pro
                565                 570                 575
Thr Tyr Phe Asn Ile Ile Pro Thr Thr Ser Arg Asp Tyr Thr Glu Leu
            580                 585                 590
Lys Phe Glu Asp Phe Gln Leu Val Asp Thr Ser Tyr Ile Tyr Ser Gly
        595                 600                 605
Gly Pro Ser Ile Ser Ser Asn Thr Leu Trp Leu Asp Asn Phe Ser Asn
    610                 615                 620
Gly Pro Val Ile Ile Asp Lys Ile Glu Phe Ile Pro Leu Gly Ile Thr
625                 630                 635                 640
Leu Asn Gln Ala Gln Gly Tyr Asp Thr Tyr Asp Gln Asn Ala Asn Gly
                645                 650                 655
Met Tyr His Gln Asn Tyr Ser Asn Ser Gly Tyr Asn Tyr Asn Gln Glu
            660                 665                 670
Tyr Asn Thr Tyr Tyr Gln Ser Tyr Asn Asn
        675                 680
```

<210> 46
<211> 529
<212> PRT
<213> Bacillus thuringiensi

<400> 46

```
Val Asn Phe Met Leu Thr Ser Gly Ala Lys Asn Met Leu Lys Leu Glu
 1                5                  10                  15
Thr Thr Asp Tyr Glu Ile Asp Gln Met Ala Asn Ala Ile Glu Asn Met
            20                  25                  30
Ser Gly Glu Gln Tyr Ser Gln Glu Lys Met Met Gln Trp His Asp Ile
        35                  40                  45
Lys Tyr Ala Lys Gln Leu Ser Gln Ala Arg Asn Leu Leu Gln Asn Gly
    50                  55                  60
Asp Phe Glu Asp Leu Phe Ser Gly Trp Thr Thr Ser Asn Gln Met Ser
65                  70                  75                  80
Ile Gln Ala Asp Asn Ala Thr Phe Lys Gly Asn Tyr Leu His Met Ser
                85                  90                  95
Gly Ala Arg Asp Ile Tyr Gly Thr Ile Phe Pro Thr Tyr Ile Tyr Gln
            100                 105                 110
Lys Ile Asp Glu Ser Lys Leu Lys Pro Tyr Thr Arg Tyr Leu Val Arg
        115                 120                 125
Gly Phe Val Gly Ser Ser Lys Asp Leu Glu Leu Met Val Met Arg Tyr
    130                 135                 140
Gly Lys Glu Ile Asp Thr Val Met Asn Val Pro Asn Asp Ile Pro Tyr
145                 150                 155                 160
Val Pro Ser Met Pro Val Cys Asn Glu Leu Tyr Asp Gly Gln Gln Pro
                165                 170                 175
Tyr Pro Asn Arg His Val Gly Tyr Tyr Asn Pro Met Pro Val Ser Gln
            180                 185                 190
Pro Ser Tyr Thr Ser Asp Thr Cys Gln Cys Thr Pro Gly Lys Lys His
        195                 200                 205
Val Val Cys His Asp Ser His Gln Phe Lys Phe His Ile Asp Thr Gly
    210                 215                 220
Glu Val Asp Tyr Asn Thr Asn Leu Gly Ile Trp Val Leu Phe Lys Ile
225                 230                 235                 240
Ser Ser Pro Asp Gly Tyr Ala Thr Leu Asp Asn Leu Glu Val Ile Glu
                245                 250                 255
Glu Gly Pro Val Arg Gly Glu Ala Val Thr His Val Lys Gln Lys Glu
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```
            260                 265                 270
Lys Lys Trp Asn Gln Gln Met Glu Lys Lys Arg Met Glu Thr Lys Arg
        275                 280                 285
Val Tyr Asp Arg Ala Lys Gln Ala Val Asp Ala Leu Phe Thr Gly Glu
    290                 295                 300
Glu Leu Asn Tyr Asp Val Thr Leu Ser His Ile Lys Asn Ala Asp Asp
305                 310                 315                 320
Leu Val Gln Ser Ile Pro Tyr Val His Asn Glu Trp Leu Pro Asp Phe
                325                 330                 335
Pro Gly Met Asn Tyr Asp Ile Tyr Gln Glu Leu Asn Ala Arg Ile Met
            340                 345                 350
Gln Ala Arg Tyr Leu Tyr Asp Ala Arg Asn Val Ile Thr Asn Gly Asp
        355                 360                 365
Phe Ala Gln Gly Leu Gln Gly Trp His Ala Glu Gly Lys Val Glu Val
    370                 375                 380
Gln Gln Met Asn Gly Thr Ser Val Leu Val Leu Ser Asn Trp Ser Ser
385                 390                 395                 400
Gly Val Ser Gln Asn Leu His Val Gln His Pro His Gly Tyr Leu Leu
                405                 410                 415
Arg Val Ser Ala Lys Lys Glu Gly Ser Gly Lys Gly Tyr Val Thr Arg
            420                 425                 430
Met Ser Cys Asn Gly Lys Gln Glu Thr Leu Thr Phe Thr Ser Cys Asp
        435                 440                 445
Gly Gly Tyr Met Thr Lys Thr Val Glu Val Phe Pro Glu Ser Asp Arg
    450                 455                 460
Val Arg Ile Glu Ile Gly Glu Thr Glu Gly Ser Phe Tyr Ile Glu Ser
465                 470                 475                 480
Ile Glu Leu Ile Cys Met Asn Gly Tyr Thr Ser Asn Asn Asn Gln Asn
                485                 490                 495
Met Ser Asn Met Tyr Asp Gln Ser Tyr Ser Gly Asn Tyr Ser Gln Asn
            500                 505                 510
Thr Ser Asp Met Tyr Asp Gln Gly Gly Ser Val Ala Lys Phe Glu Lys
        515                 520                 525
Glu
```

<210> 47
<211> 674
<212> PRT
<213> Bacillus thuringiensi

<400> 47

```
Met Asn Gln Tyr Gln Asn Lys Asn Glu Tyr Glu Ile Leu Glu Ser Ser
 1               5                  10                  15
Gln Asn Asn Met Asn Met Pro Asn Arg Tyr Pro Phe Ala Asp Asp Pro
            20                  25                  30
Asn Ala Val Met Lys Asn Gly Asn Tyr Lys Asp Trp Val Asn Glu Cys
        35                  40                  45
Glu Gly Ser Asn Ile Ser Pro Ser Pro Ala Ala Ala Ile Thr Ser Lys
    50                  55                  60
Ile Val Ser Ile Val Leu Lys Thr Leu Ala Lys Ala Val Ala Ser Ser
65                  70                  75                  80
Leu Ala Asp Ser Ile Lys Ser Ser Leu Gly Ile Ser Lys Thr Ile Thr
                85                  90                  95
Glu Asn Asn Val Ser Gln Val Ser Met Val Gln Val His Gln Ile Ile
            100                 105                 110
Asn Arg Arg Ile Gln Glu Thr Ile Leu Asp Leu Gly Glu Ser Ser Leu
        115                 120                 125
Asn Gly Leu Val Ala Ile Tyr Asn Arg Asp Tyr Leu Gly Ala Leu Glu
    130                 135                 140
Ala Trp Asn Asn Asn Lys Ser Asn Ile Asn Tyr Gln Thr Asn Val Ala
145                 150                 155                 160
Glu Ala Phe Lys Thr Val Glu Arg Glu Phe Phe Thr Lys Leu Lys Gly
                165                 170                 175
Ile Tyr Arg Thr Ser Ser Ser Gln Ile Thr Leu Leu Pro Thr Phe Thr
            180                 185                 190
Gln Ala Ala Asn Leu His Leu Ser Met Leu Arg Asp Ala Val Met Tyr
```

```
        195                 200                 205
Gln Glu Gly Trp Asn Leu Gln Ser His Ile Asn Tyr Ser Lys Glu Leu
    210                 215                 220
Asp Asp Ala Leu Glu Asp Tyr Thr Asn Tyr Cys Val Glu Val Tyr Thr
225                 230                 235                 240
Lys Gly Leu Asn Ala Leu Arg Gly Ser Thr Ala Ile Asp Trp Leu Glu
                245                 250                 255
Phe Asn Ser Phe Arg Arg Asp Met Thr Leu Met Val Leu Asp Leu Val
            260                 265                 270
Ala Ile Phe Pro Asn Tyr Asn Pro Val Arg Tyr Pro Leu Ser Thr Lys
        275                 280                 285
Ile Ser Leu Ser Arg Lys Ile Tyr Thr Asp Pro Val Gly Arg Thr Asp
    290                 295                 300
Ser Pro Ser Phe Gly Asp Trp Thr Asn Thr Gly Arg Thr Leu Ala Asn
305                 310                 315                 320
Phe Asn Asp Leu Glu Arg Glu Val Thr Asp Ser Pro Ser Leu Val Lys
                325                 330                 335
Trp Leu Gly Asp Met Thr Ile Tyr Thr Gly Ala Ile Asp Ser Tyr Arg
            340                 345                 350
Pro Thr Ser Pro Gly Asp Arg Ile Gly Val Trp Tyr Gly Asn Ile Asn
        355                 360                 365
Ala Phe Tyr His Thr Gly Arg Thr Asp Val Val Met Phe Arg Gln Thr
    370                 375                 380
Gly Asp Thr Ala Tyr Glu Asp Pro Ser Thr Phe Ile Ser Asn Ile Leu
385                 390                 395                 400
Tyr Asp Asp Ile Tyr Lys Leu Asp Leu Arg Ala Ala Ala Val Ser Thr
                405                 410                 415
Ile Gln Gly Ala Met Asp Thr Thr Phe Gly Val Ser Ser Ser Arg Phe
            420                 425                 430
Phe Asp Ile Arg Gly Arg Asn Gln Leu Tyr Gln Ser Asn Lys Pro Tyr
        435                 440                 445
Pro Ser Leu Pro Ile Thr Ile Thr Phe Pro Gly Glu Glu Ser Ser Glu
    450                 455                 460
Gly Asn Ala Asn Asp Tyr Ser His Leu Leu Cys Asp Val Lys Ile Leu
465                 470                 475                 480
Gln Glu Asp Ser Ser Asn Ile Cys Glu Gly Arg Ser Ser Leu Leu Ser
                485                 490                 495
His Ala Trp Thr His Ala Ser Leu Asp Arg Asn Asn Thr Ile Leu Pro
            500                 505                 510
Asp Glu Ile Thr Gln Ile Pro Ala Val Thr Ala Tyr Glu Leu Arg Gly
        515                 520                 525
Asn Ser Ser Val Val Ala Gly Pro Gly Ser Thr Gly Gly Asp Leu Val
    530                 535                 540
Lys Met Ser Tyr His Ser Val Trp Ser Phe Lys Val Tyr Cys Ser Glu
545                 550                 555                 560
Leu Lys Asn Tyr Arg Val Arg Ile Arg Tyr Ala Ser His Gly Asn Cys
                565                 570                 575
Gln Phe Leu Met Lys Arg Trp Pro Ser Thr Gly Val Ala Pro Arg Gln
            580                 585                 590
Trp Ala Arg His Asn Val Gln Gly Thr Phe Ser Asn Ser Met Arg Tyr
        595                 600                 605
Glu Ala Phe Lys Tyr Leu Asp Ile Phe Thr Ile Thr Pro Glu Glu Asn
    610                 615                 620
Asn Phe Ala Phe Thr Ile Asp Leu Glu Ser Gly Gly Asp Leu Phe Ile
625                 630                 635                 640
Asp Lys Ile Glu Phe Ile Pro Val Ser Gly Ser Ala Phe Glu Tyr Glu
                645                 650                 655
Gly Lys Gln Asn Ile Glu Lys Thr Gln Lys Ala Val Asn Asp Leu Phe
            660                 665                 670
Ile Asn
```

<210> 48
<211> 675
<212> PRT
<213> Bacillus thuringiensi

<400> 48
Met Asn Pro Tyr Gln Asn Lys Ser Glu Cys Glu Ile Leu Asn Ala Pro
1 5 10 15
Leu Asn Asn Ile Asn Met Pro Asn Arg Tyr Pro Phe Ala Asn Asp Pro
20 25 30
Asn Ala Val Met Lys Asn Gly Asn Tyr Lys Asp Trp Leu Asn Glu Cys
35 40 45
Asp Gly Ile Thr Pro Ser Ile Phe Gly Thr Leu Gly Val Leu Ala Ser
50 55 60
Ile Val Ile Ser Thr Ile Asn Leu Ala Thr Ser Pro Ser Ile Gly Asp
65 70 75 80
Ala Phe Ala Leu Val Ser Ser Ile Gly Glu Tyr Trp Pro Glu Thr Lys
85 90 95
Thr Ser Phe Pro Leu Ser Val Ala Asp Val Asn Arg Leu Ile Arg Glu
100 105 110
Ala Leu Asp Gln Asn Ala Ile Asn Arg Ala Thr Gly Lys Phe Asn Gly
115 120 125
Leu Met Asp Thr Tyr Asn Thr Val Tyr Leu Lys Asn Leu Gln Asp Trp
130 135 140
Tyr Asp Thr Arg Ile Pro Ala Asn Pro Gln Gly Asp Ser Gln Leu Arg
145 150 155 160
Glu Ala Ala Arg Arg Ser Leu Glu Glu Ile Glu Arg Asp Phe Arg Lys
165 170 175
Ala Leu Ala Gly Glu Phe Ala Glu Ala Gly Ser Gln Ile Val Leu Leu
180 185 190
Pro Ile Tyr Ala Gln Ala Ala Asn Ile His Leu Leu Ile Leu Lys Asp
195 200 205
Ala Met Gln Phe Arg Thr Asp Leu Gly Leu Ile Arg Pro Val Gly Val
210 215 220
Pro Ile Thr Thr Ser Ala Glu Asp Pro Phe Glu Ser Glu Phe Leu Leu
225 230 235 240
Arg Ile Lys Lys Tyr Thr Asp His Cys Ile Ser Tyr Tyr Asp Asp Gly
245 250 255
Leu Ala Lys Ile Arg Ser Arg Gly Ser Asp Gly Glu Thr Trp Trp Glu
260 265 270
Phe Asn Lys Phe Arg Arg Glu Met Thr Leu Thr Val Leu Asp Leu Val
275 280 285
Ala Leu Tyr Pro Thr His Asn Ile Lys Leu Tyr Pro Ile Pro Thr Gln
290 295 300
Thr Glu Leu Ser Arg Val Val Tyr Thr Asp Pro Val Gly Cys Phe Gly
305 310 315 320
Asn Arg Lys Ser Asp Ile Phe Ser Arg Leu Asn Phe Asp Tyr Leu Glu
325 330 335
Asn Arg Leu Thr Arg Pro Arg Glu Pro Phe Asn Tyr Leu Asn Ser Val
340 345 350
Gln Leu Phe Ala Ser Thr Val Ser Asn Ser Asn Asn Gly Glu Val Leu
355 360 365
Arg Gly Asn Leu Asn Lys Ile Met Phe Glu Gly Gly Trp Thr Ala Ser
370 375 380
Arg Ser Gly Asp Gly Val Thr Thr Gly Thr Pro Phe Ser Thr Met Asp
385 390 395 400
Trp Ser Tyr Gly Trp Gly Tyr Pro Arg Lys His Tyr Ala Glu Ile Thr
405 410 415
Ser Arg Ser Gln Ala Leu Pro Gly Leu Asn Asn Ser Ile His Val Ile
420 425 430
Val Gly Ile Asp Ser Phe Arg Ala Ile Gly Pro Gly Gly Gln Gly Asp
435 440 445
His Thr Phe Ser Leu Pro Gly Gly Asp Met Tyr Asp Cys Gly Lys Val
450 455 460
Gln Ile Asn Pro Leu Glu Asp Tyr Arg Asn Ser Asp His Trp Ile Ser
465 470 475 480
Asp Met Met Thr Ile Asn Gln Ser Val Gln Leu Ala Ser Asn Pro Thr
485 490 495
Gln Thr Phe Ala Phe Ser Ala Leu Ser Leu Gly Trp His His Ser Ser
500 505 510
Ala Gly Asn Arg Asn Val Tyr Val Tyr Asp Lys Ile Thr Gln Ile Pro
515 520 525
Ala Thr Lys Thr Val Arg Glu His Pro Met Ile Lys Gly Pro Gly Phe

```
    530                 535                 540
Thr Gly Gly Asp Leu Ala Asp Leu Ser Ser Asn Ser Asp Ile Leu Gln
545                 550                 555                 560
Tyr Asp Leu Arg Ser Asp Tyr Asp Asp Arg Leu Thr Glu Asp Val Pro
                565                 570                 575
Phe Arg Ile Arg Ile Arg Cys Ala Ser Ile Gly Val Ser Thr Ile Ser
            580                 585                 590
Val Asp Asn Trp Gly Ser Ser Ser Pro Gln Val Thr Val Ala Ser Thr
        595                 600                 605
Ala Ala Ser Leu Asp Thr Leu Lys Tyr Glu Ser Phe Gln Tyr Val Ser
    610                 615                 620
Ile Pro Gly Asn Tyr Tyr Phe Asp Ser Ala Pro Arg Ile Arg Leu Leu
625                 630                 635                 640
Arg Gln Pro Gly Arg Leu Leu Val Asp Arg Ile Glu Ile Ile Pro Val
                645                 650                 655
Asn Phe Phe Pro Leu Ser Glu Gln Glu Asn Lys Ser Val Asp Ser Leu
            660                 665                 670
Phe Ile Asn
        675
```

<210> 49
<211> 659
<212> PRT
<213> Bacillus thuringiensi

```
<400> 49
Asn Ser Tyr Glu Asn Lys Asn Glu Tyr Glu Ile Leu Asn Asp Ser Lys
 1               5                  10                  15
Lys Ser Asn Met Ser Asn Pro Tyr Leu Arg Tyr Pro Leu Ala Asn Asp
            20                  25                  30
Ser Leu Ala Ser Met Gln Asn Thr Asn Tyr Lys Asp Trp Leu Thr Met
        35                  40                  45
Cys Asp Arg Thr Asp Thr Asp Val Leu Ser Ser Arg Gly Ala Val Ser
    50                  55                  60
Thr Gly Val Gly Met Leu Ser Thr Ile Leu Ser Leu Phe Gly Ile Pro
65                  70                  75                  80
Leu Ile Gly Glu Gly Ile Asp Leu Leu Leu Gly Ala Ala Asp Phe Leu
                85                  90                  95
Trp Pro Glu Ser Asp Gly Gly His Gln Tyr Thr Trp Glu Asp Leu Met
            100                 105                 110
Asn His Ile Glu Glu Leu Met Asp Glu Arg Leu Glu Thr Glu Lys Arg
        115                 120                 125
Thr Thr Ala Leu Asp Asp Leu Arg Gly Leu Lys Ala Leu Leu Gly Leu
    130                 135                 140
Phe Arg Asp Ala Phe Asp Ser Trp Glu Lys Asn Gln Asn Asp Pro Ile
145                 150                 155                 160
Ala Lys Asn Arg Val Gly Gly Tyr Phe Glu Asp Val His Thr His Phe
                165                 170                 175
Val Lys Asp Met Ala Ser Ile Phe Ser Ala Thr Asn Tyr Glu Val Leu
            180                 185                 190
Leu Leu Pro Val Tyr Ala Gln Ala Ala Asn Leu His Leu Leu Leu Leu
        195                 200                 205
Arg Glu Gly Val Ile Tyr Gly Ser Arg Trp Gly Ile Ala Pro Ala Ala
    210                 215                 220
Asp Phe Tyr His Asp Gln Leu Leu Lys Tyr Thr Ala Ile Tyr Ala Asn
225                 230                 235                 240
His Cys Val Thr Trp Tyr Asn Asn Gly Leu Ala Gln Gln Lys Glu Leu
                245                 250                 255
Phe Ala Lys Ser Pro Asn Trp Asn Arg Phe Asn Ala Tyr Arg Arg Asp
            260                 265                 270
Met Thr Ile Thr Val Leu Asp Ile Ile Ala Leu Phe Pro Thr Tyr Asp
        275                 280                 285
Ala Arg Leu Tyr Thr Lys Pro Ile Lys Thr Glu Leu Thr Arg Glu Ile
    290                 295                 300
Tyr Ser Asp Val Leu Asn Leu Asp Val Tyr Gly Val Gln Gln Thr Asp
305                 310                 315                 320
Leu Asn Lys Asn Glu Ala Ala Phe Thr Arg Ser Pro His Leu Val Thr
```

```
                325                 330                 335
Arg Leu Arg Gly Phe Asp Phe Tyr Thr Arg Thr Lys Tyr Ala Tyr Trp
            340                 345                 350
Arg Tyr Leu Ala Gly His Thr Asn Tyr Phe Ser Phe Thr Gly Asn Gly
        355                 360                 365
Thr Ile Tyr Ser Ser Ser Phe Asn Asn Trp Tyr Asp Thr Asp Met Thr
    370                 375                 380
Lys Ser Thr Ile Asn Ile Pro Asp Tyr Ala Asn Ile Tyr Lys Leu Trp
385                 390                 395                 400
Thr Lys Ser Tyr Thr Asn Ile Ser Pro Tyr Thr Asp Pro Val Gly Ile
                405                 410                 415
Ser Gln Met Gln Phe Ser Leu Thr Asn Asn Gln Gln Leu Thr Tyr Thr
            420                 425                 430
Gly Thr Ser Ala Pro Lys Tyr Pro Val Arg Glu Thr Phe Phe Glu Ile
        435                 440                 445
Pro Pro Thr Asp Glu Lys Pro Leu Thr Tyr Glu Asn Tyr Ser His Ile
    450                 455                 460
Leu Ser Tyr Met Thr Ser Ala Gln His Phe Gly Asp Lys Lys Ile Gly
465                 470                 475                 480
Tyr Thr Phe Ala Trp Met His Glu Ser Val Asp Phe Asp Asn Arg Val
                485                 490                 495
Asp Pro Asp Lys Ile Thr Gln Ile Pro Ala Val Lys Gly Asp Tyr Leu
            500                 505                 510
Gln Tyr Gly Tyr Val Lys Gln Gly Pro Gly His Thr Gly Gly Asp Leu
        515                 520                 525
Val Ser Met Ile Arg Thr Asp Arg Leu Gly Ile Asn Val Tyr Phe Pro
    530                 535                 540
Gln Pro Leu Asp Tyr Arg Ile Arg Ile Arg Tyr Ser Thr Ser Ser Asn
545                 550                 555                 560
Gly Tyr Leu Tyr Ile Tyr Ser Pro Asn Thr Lys Ile Val Tyr Leu Pro
                565                 570                 575
Pro Thr Thr Leu Val Asp Gly Gln Pro Thr Phe Asp Pro Met Asp Phe
            580                 585                 590
Ser Ala Phe Arg Val Val Glu Val Pro Ala Ser Phe Arg Ala Ser Val
        595                 600                 605
Ala Gly Tyr Thr Asn Phe Thr Ile Glu Ala Gly Phe Gly Pro Val Tyr
    610                 615                 620
Ile Asp Lys Ile Glu Phe Ile Pro Asp Asn Thr Thr Thr Leu Glu Tyr
625                 630                 635                 640
Glu Gly Gly Arg Asp Leu Glu Lys Thr Lys Asn Ala Val Asn Asp Leu
                645                 650                 655
Phe Thr Asn
```

<210> 50
<211> 558
<212> PRT
<213> Bacillus thuringiensi

<400> 50

```
Met Phe Ile Ser Asn Ile Lys Asn Thr Leu Lys Ile Glu Thr Thr Asp
 1               5                  10                  15
Tyr Glu Ile Asp Gln Ala Ala Ile Ser Ile Glu Cys Met Ser Asn Glu
            20                  25                  30
His Ser Ser Lys Glu Glu Met Met Leu Trp Asp Glu Val Lys Gln Ala
        35                  40                  45
Lys Gln Leu Ser Trp Ser Arg Asn Leu Leu Tyr Asn Gly Asp Phe Glu
    50                  55                  60
Asp Val Ser Asn Gly Trp Lys Thr Ser Asn Thr Ile Glu Ile Arg Glu
65                  70                  75                  80
Asn Ser Pro Val Phe Lys Gly His Tyr Leu His Met Phe Gly Ala Arg
                85                  90                  95
Asp Ile Asp Gly Thr Leu Phe Pro Thr Tyr Ile Tyr Gln Lys Ile Glu
            100                 105                 110
Glu Ser Lys Leu Lys Pro Tyr Thr Arg Tyr Arg Val Arg Gly Phe Val
        115                 120                 125
Gly Ser Ser Lys Asp Leu Lys Leu Met Val Thr Arg Tyr Gly Lys Glu
```

```
    130                 135                 140
Ile Asp Ala Met Met Asn Val Pro Asn Asp Leu Ala Tyr Met Gln Pro
145                 150                 155                 160
Thr Pro Ser Cys Gly Asp Ser Arg Cys Glu Ser Ser Ser Arg Tyr Val
                165                 170                 175
Ser Gln Gly Tyr Pro Thr Pro Val Thr Asp Gly Tyr Ala Ser Gly Arg
            180                 185                 190
Tyr Ala Cys Gln Ser Asn Arg Gly Thr Lys His Val Lys Cys His Asp
        195                 200                 205
Arg His Pro Phe Asp Phe His Ile Asp Thr Gly Glu Leu Asp Thr Asn
    210                 215                 220
Thr Asn Val Gly Ile Asp Val Leu Phe Lys Ile Ser Asn Pro Asp Gly
225                 230                 235                 240
Tyr Ala Thr Leu Gly Asn Leu Glu Val Ile Glu Glu Gly Pro Leu Thr
                245                 250                 255
Gly Glu Ala Leu Thr His Val Lys Gln Lys Glu Lys Lys Trp Lys Gln
            260                 265                 270
His Met Glu Lys Lys Arg Trp Glu Thr Gln Gln Ala Tyr Asp Pro Ala
        275                 280                 285
Lys Gln Ala Val Asp Ala Leu Phe Thr Asn Glu Gln Glu Leu His Tyr
    290                 295                 300
His Ile Thr Leu Asp His Ile Gln Asn Ala Asp Arg Leu Ile Gln Ala
305                 310                 315                 320
Ile Pro Tyr Val Tyr His Ala Trp Leu Pro Asp Ala Pro Gly Met Asn
                325                 330                 335
Tyr Asp Gly Tyr Gln Gly Leu Asn Ala Arg Ile Met Gln Ala Tyr Asn
            340                 345                 350
Leu Tyr Asp Ala Arg Asn Val Ile Thr Asn Gly Asp Phe Thr Gln Gly
        355                 360                 365
Leu Thr Gly Trp His Ala Ala Gly Lys Ala Met Val Gln Gln Met Asp
    370                 375                 380
Gly Ala Ser Val Leu Val Leu Ser Asn Trp Ser Ala Gly Val Ser Gln
385                 390                 395                 400
Asn Leu His Val Gln Glu His His Gly Tyr Met Leu Arg Val Ile Ala
                405                 410                 415
Lys Lys Glu Gly Pro Gly Lys Gly Tyr Val Thr Met Met Asp Cys Asn
            420                 425                 430
Gly Asn Arg Glu Thr Leu Lys Phe Thr Ser Cys Glu Glu Gly Tyr Met
        435                 440                 445
Thr Lys Thr Val Glu Val Phe Pro Glu Ser Asp Arg Val Arg Ile Glu
    450                 455                 460
Ile Gly Glu Thr Glu Gly Thr Phe Tyr Val Asp Ser Ile Glu Leu Leu
465                 470                 475                 480
Cys Met Gln Gly Tyr Ala Ser Asn Asn Asn Pro His Thr Gly Asn Met
                485                 490                 495
Tyr Gly Gln Ser Tyr Asn Gly Asn Tyr Asn Gln Asn Thr Ser Asp Val
            500                 505                 510
Tyr His Gln Gly Tyr Thr Asn Asn Tyr Asn Gln Asn Ser Ser Asn Met
        515                 520                 525
Tyr Asn Gln Asn Tyr Thr His Asn Asp Asp Leu His Ser Gly Cys Thr
    530                 535                 540
Cys Asn Gln Gly His Asn Ser Gly Cys Thr Cys Ser Gln Gly
545                 550                 555
```

<210> 51
<211> 666
<212> PRT
<213> Bacillus thuringiensi

<400> 51

```
Asn Ser Tyr Glu Asn Lys Asn Glu Tyr Glu Ile Leu Glu Ser Ser Ser
 1               5                  10                  15
Asn Asn Thr Asn Met Pro Asn Arg Tyr Pro Phe Ala Asn Asp Arg Asp
            20                  25                  30
Met Ser Thr Met Ser Phe Asn Asp Cys Gln Gly Ile Ser Trp Asp Glu
        35                  40                  45
Ile Trp Glu Ser Ala Glu Thr Ile Thr Ser Ile Gly Ile Asp Leu Ile
```

```
    50                  55                  60
Glu Phe Leu Met Glu Pro Ser Leu Gly Gly Ile Asn Thr Leu Phe Ser
65                  70                  75                  80
Ile Ile Gly Lys Leu Ile Pro Thr Asn His Gln Ser Val Ser Ala Leu
                85                  90                  95
Ser Ile Cys Asp Leu Leu Ser Ile Ile Arg Lys Glu Val Ala Asp Ser
            100                 105                 110
Val Leu Ser Asp Ala Ile Cys Arg Phe Leu Asp Gly Lys Leu Lys Asn
        115                 120                 125
Tyr Arg Glu Tyr Tyr Leu Pro Tyr Leu Glu Ala Trp Leu Lys Asp Gly
    130                 135                 140
Lys Pro Leu Gln Lys Thr Asn Asn Ser Asp Ile Gly Gln Leu Val Lys
145                 150                 155                 160
Tyr Phe Glu Leu Ser Glu Arg Asp Phe Asn Glu Ile Leu Gly Gly Ser
                165                 170                 175
Leu Ala Arg Asn Asn Ala Gln Ile Leu Leu Leu Pro Tyr Phe Cys Ala
            180                 185                 190
Ser Cys Lys Cys Gln Leu Leu Leu Leu Arg Asp Ala Val Gln Tyr Glu
        195                 200                 205
Glu Gln Trp Phe Pro Phe Leu Ser Ala Glu Asn Val Arg Ser Glu Leu
    210                 215                 220
Ile Ser Pro Asn Ser Gly Cys Asp Phe Thr Gly Asp Tyr Tyr Glu Arg
225                 230                 235                 240
Leu Lys Cys Lys Ile Ala Glu Tyr Thr Asp Tyr Cys Glu Tyr Trp Tyr
                245                 250                 255
Gln Ala Gly Leu Asn Gln Ile Lys Gln Ala Gly Thr Gly Ala Asp Thr
            260                 265                 270
Trp Ala Lys Phe Asn Lys Phe Arg Arg Glu Met Thr Leu Thr Val Leu
        275                 280                 285
Asp Ile Ile Ala Ile Phe Gln Thr Tyr Asp Phe Lys Lys Tyr Pro Leu
    290                 295                 300
Pro Thr His Val Glu Leu Thr Arg Glu Ile Tyr Thr Asp Pro Val Gly
305                 310                 315                 320
Tyr Ser Ser Gly Thr Tyr Ser Trp Leu Lys Tyr Trp Thr Gly Ala Phe
                325                 330                 335
Asn Thr Leu Glu Ala Asn Gly Thr Arg Gly Pro Gly Leu Val Thr Trp
            340                 345                 350
Leu Arg Ser Ile Gly Ile Tyr Asn Glu Tyr Val Ser Arg Tyr Phe Ser
        355                 360                 365
Gly Trp Val Gly Thr Arg His Tyr Glu Asp Tyr Thr Thr Gly Asn Gly
    370                 375                 380
Asn Phe Gln Arg Met Ser Gly Thr Thr Ser Asn Asp Leu Arg Asp Ile
385                 390                 395                 400
Ser Phe Pro Asn Ser Asp Ile Phe Lys Ile Glu Ser Lys Ala Ile Met
                405                 410                 415
Asn Leu Val Gly Glu Ile Asn Ala Arg Pro Glu Tyr Arg Val Ser Arg
            420                 425                 430
Ala Glu Phe Ser Glu Ser Thr Ala Phe Ile Tyr Leu Tyr Asp Ala Gly
        435                 440                 445
Asn Ser Gly Leu Ser Ser Met Thr Ile Thr Ser Lys Leu Pro Gly Ile
    450                 455                 460
Lys Asn Pro Glu Pro Ser Tyr Arg Asp Tyr Ser His Arg Leu Ser Asn
465                 470                 475                 480
Ala Ala Cys Val Gly Ala Gly Asn Ser Arg Ile Asn Val Tyr Gly Trp
                485                 490                 495
Thr His Thr Ser Met Ser Lys Tyr Asn Leu Ile Tyr Pro Asp Lys Ile
            500                 505                 510
Thr Gln Ile Pro Ala Val Lys Ala Phe Asp Ile Ser Asp Thr Gly Pro
        515                 520                 525
Gly Gln Val Ile Ala Gly Pro Gly His Thr Gly Gly Asn Val Val Ser
    530                 535                 540
Leu Pro Tyr Tyr Ser Arg Leu Lys Ile Arg Leu Ile Pro Ala Ser Thr
545                 550                 555                 560
Asn Lys Asn Tyr Leu Val Arg Val Arg Tyr Thr Ser Thr Ser Asn Gly
                565                 570                 575
Arg Leu Leu Val Glu Arg Trp Ser Pro Ser Ser Ile Ile Asn Ser Tyr
            580                 585                 590
Phe Phe Leu Pro Ser Thr Gly Pro Gly Asp Ser Phe Gly Tyr Val Asp
```

```
        595                 600                 605
Thr Leu Val Thr Thr Phe Asn Gln Pro Gly Val Glu Ile Ile Ile Gln
    610                 615                 620
Asn Leu Asp Thr Pro Ile Asn Val Asp Lys Val Glu Phe Ile Pro Val
625                 630                 635                 640
Asn Ser Thr Ala Leu Glu Tyr Glu Gly Lys Gln Ser Leu Glu Lys Ala
                645                 650                 655
Gln Asp Val Val Asn Asp Leu Phe Val Lys
            660                 665
```

<210> 52
<211> 558
<212> PRT
<213> Bacillus thuringiensi

<400> 52

```
Met Phe Thr Asn Gly Thr Lys Asn Thr Leu Lys Ile Glu Thr Thr Asp
 1               5                  10                  15
Tyr Glu Ile Asp Gln Ala Ala Ile Ser Ile Glu Cys Met Ser Asp Glu
            20                  25                  30
His Ser Pro Lys Glu Lys Met Met Leu Trp Asp Glu Val Lys Arg Ala
        35                  40                  45
Lys Leu Leu Ser Gln Ser Arg Asn Leu Leu Gln Asn Gly Asp Phe Gly
    50                  55                  60
Asp Phe Tyr Gly Asn Asp Trp Lys Phe Gly Asn Asn Ile Ile Ile Gly
65                  70                  75                  80
Ser Asn Asn Ser Ile Phe Lys Gly Asn Phe Leu Gln Met Ser Gly Ala
                85                  90                  95
Arg Asp Ile Tyr Gly Thr Ile Phe Pro Thr Tyr Ile Tyr Gln Lys Ile
            100                 105                 110
Asp Glu Ser Lys Leu Lys Pro Tyr Thr Arg Tyr Arg Val Arg Gly Phe
        115                 120                 125
Val Gly Ser Ser Lys Asp Leu Arg Leu Met Val Thr Arg Tyr Gly Lys
    130                 135                 140
Glu Ile Asp Ala Met Met Asn Val Pro Asn Asp Leu Ala Tyr Met Gln
145                 150                 155                 160
Pro Asn Pro Ser Cys Gly Asp Ser Arg Cys Glu Ser Ser Ser Gln Tyr
                165                 170                 175
Val Ser Gln Gly Tyr Pro Thr Pro Thr Asp Gly Tyr Ala Pro Asp Arg
            180                 185                 190
Tyr Ala Cys Pro Ser Ser Ser Asp Lys Lys His Val Met Cys His Asp
        195                 200                 205
Arg His Pro Phe Asp Phe His Ile Asp Thr Gly Glu Leu Asp Thr Asn
    210                 215                 220
Thr Asn Val Gly Ile Asp Val Leu Phe Lys Ile Ser Asn Pro Asp Gly
225                 230                 235                 240
Tyr Ala Thr Leu Gly Asn Leu Glu Val Ile Glu Glu Gly Pro Leu Thr
                245                 250                 255
Gly Glu Ala Leu Thr His Val Lys Gln Lys Glu Lys Lys Trp Lys Gln
            260                 265                 270
His Met Glu Lys Lys Arg Trp Glu Thr Gln Gln Ala Tyr Asp Pro Ala
        275                 280                 285
Lys Gln Ala Val Asp Thr Leu Phe Thr Asn Glu Gln Glu Leu His Tyr
    290                 295                 300
His Ile Thr Leu Asp Tyr Ile Gln Thr Leu Ile Asp Trp Tyr Ser Arg
305                 310                 315                 320
Phe Pro Ile Tyr Thr Met Thr Gly Tyr Arg Asp Ala Pro Gly Met Asn
                325                 330                 335
Tyr Asp Gly Tyr Gln Gly Leu Asn Ala Arg Ile Met Gln Ala Tyr Asn
            340                 345                 350
Leu Tyr Asp Ala Arg Asn Val Ile Thr Asn Gly Asp Phe Thr Lys Gly
        355                 360                 365
Leu Gln Gly Trp His Ala Ala Gly Lys Ala Ala Val Gln Gln Ile Asp
    370                 375                 380
Gly Ala Ser Val Leu Val Leu Ser Asn Trp Ser Ala Gly Val Ser Gln
385                 390                 395                 400
Asn Leu His Ala Gln Asp His His Gly Tyr Met Leu Arg Val Ile Ala
```

```
                405                 410                 415
Lys Lys Glu Gly Pro Gly Lys Gly Tyr Val Thr Met Met Asp Cys Asn
            420                 425                 430
Gly Asn Gln Glu Thr Leu Lys Phe Thr Ser Cys Glu Glu Gly Tyr Met
        435                 440                 445
Thr Lys Thr Val Glu Val Phe Pro Glu Ser Asp Arg Val Arg Ile Glu
    450                 455                 460
Ile Gly Glu Thr Glu Gly Thr Phe Tyr Val Asp Ser Ile Glu Leu Leu
465                 470                 475                 480
Cys Met Gln Gly Tyr Ala Ser Asn Asn Asn Pro His Thr Gly Asn Met
                485                 490                 495
Tyr Gly Gln Ser Tyr Asn Gly Asn Tyr Asn Gln Asn Thr Ser Asp Val
            500                 505                 510
Tyr His Gln Gly Tyr Thr Asn Asn Tyr Asn Gln Asn Ser Ser Asn Met
        515                 520                 525
Tyr Asn Gln Asn Tyr Thr His Asn Asp Asp Leu His Ser Gly Cys Thr
    530                 535                 540
Cys Asn Gln Gly His Asn Ser Gly Cys Thr Cys Ser Gln Gly
545                 550                 555
```